



Sequence Listing

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<10> Baker, Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
Pan, James
Paoni, Nicholas F.

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aaaaaaaaa 1508

<210> 10
<211> 319
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-17
<223> Signal Peptide

<220>
<221> misc_feature
<222> 36-47, 108-113, 166-171, 198-203, 207-212
<223> N-myristoylation Sites.

<220>
<221> misc_feature
<222> 39-42
<223> Glycosaminoglycan Attachment Site.

<220>
<221> TRANSMEM
<222> 136-152
<223> Transmembrane Domain

<220>
<221> misc_feature
<222> 161-163, 187-190 and 253-256
<223> N-glycosylation Sites.

<400> 10
Met Leu Phe Trp Val Leu Gly Leu Leu Ile Leu Cys Gly Phe Leu
1 5 10 15

Trp Thr Arg Lys Gly Lys Leu Lys Ile Glu Asp Ile Thr Asp Lys
20 25 30

Tyr Ile Phe Ile Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Ala
35 40 45

Ala Arg Thr Phe Asp Lys Lys Gly Phe His Val Ile Ala Ala Cys
50 55 60

Leu Thr Glu Ser Gly Ser Thr Ala Leu Lys Ala Glu Thr Ser Glu
65 70 75

Arg Leu Arg Thr Val Leu Leu Asp Val Thr Asp Pro Glu Asn Val
80 85 90

Lys Arg Thr Ala Gln Trp Val Lys Asn Gln Val Gly Glu Lys Gly
95 100 105

Leu Trp Gly Leu Ile Asn Asn Ala Gly Val Pro Gly Val Leu Ala
110 115 120

Pro Thr Asp Trp Leu Thr Leu Glu Asp Tyr Arg Glu Pro Ile Glu
 125 130 135

 Val Asn Leu Phe Gly Leu Ile Ser Val Thr Leu Asn Met Leu Pro
 140 145 150

 Leu Val Lys Lys Ala Gln Gly Arg Val Ile Asn Val Ser Ser Val
 155 160 165

 Gly Gly Arg Leu Ala Ile Val Gly Gly Tyr Thr Pro Ser Lys
 170 175 180

 Tyr Ala Val Glu Gly Phe Asn Asp Ser Leu Arg Arg Asp Met Lys
 185 190 195

 Ala Phe Gly Val His Val Ser Cys Ile Glu Pro Gly Leu Phe Lys
 200 205 210

 Thr Asn Leu Ala Asp Pro Val Lys Val Ile Glu Lys Lys Leu Ala
 215 220 225

 Ile Trp Glu Gln Leu Ser Pro Asp Ile Lys Gln Gln Tyr Gly Glu
 230 235 240

 Gly Tyr Ile Glu Lys Ser Leu Asp Lys Leu Lys Gly Asn Lys Ser
 245 250 255

 Tyr Val Asn Met Asp Leu Ser Pro Val Val Glu Cys Met Asp His
 260 265 270

 Ala Leu Thr Ser Leu Phe Pro Lys Thr His Tyr Ala Ala Gly Lys
 275 280 285

 Asp Ala Lys Ile Phe Trp Ile Pro Leu Ser His Met Pro Ala Ala
 290 295 300

 Leu Gln Asp Phe Leu Leu Leu Lys Gln Lys Ala Glu Leu Ala Asn
 305 310 315

 Pro Lys Ala Val

<210> 11
 <211> 2720
 <212> DNA
 <213> Homo sapines

<400> 11
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 gccccttggg ccgtcgccac cactgttagtc atgtacccac cgccgcccggc 150

 gccgcctcat cgggacttca tctcggtgac gctgagcttt ggcgagagct 200

atgacaacag caagagttgg cggcggcgct cgtgctggag gaaatggaag 250
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cgcgctggac accatgtgga tcttgggtct gagaaaaagaa tttgaggaag 950
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aacctgtttg agagcacgat ccgcacatcctg gggggctcc tgagtgccta 1050
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tgtccaggat cctcagaagc ccgagcctag ggacaagatg gagagcttct 2000
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gcctgaggct ccagggctgg ctctgggttt tacaagctgg actcaggat 2600
cctcctggcc gccccgcagg gggcttggag ggctggacgg caagtccgtc 2650
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ttgatttgct ctaaccgcaa 2720

<210> 12
<211> 699
<212> PRT
<213> Homo sapiens

<220>
<221> TRANSMEM
<222> 21-40 and 84-105
<223> Transmembrane Domain (type II)

<400> 12
Met Ala Ala Cys Glu Gly Arg Arg Ser Gly Ala Leu Gly Ser Ser

1 5 10 15
Gln Ser Asp Phe Leu Thr Pro Pro Val Gly Gly Ala Pro Trp Ala
20 25 30
Val Ala Thr Thr Val Val Met Tyr Pro Pro Pro Pro Pro Pro Pro
35 40 45
His Arg Asp Phe Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr
50 55 60
Asp Asn Ser Lys Ser Trp Arg Arg Ser Cys Trp Arg Lys Trp
65 70 75
Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu
80 85 90
Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala
95 100 105
Asp His Trp Lys Ala Leu Ala Phe Arg Leu Glu Glu Glu Gln Lys
110 115 120
Met Arg Pro Glu Ile Ala Gly Leu Lys Pro Ala Asn Pro Pro Val
125 130 135
Leu Pro Ala Pro Gln Lys Ala Asp Thr Asp Pro Glu Asn Leu Pro
140 145 150
Glu Ile Ser Ser Gln Lys Thr Gln Arg His Ile Gln Arg Gly Pro
155 160 165
Pro His Leu Gln Ile Arg Pro Pro Ser Gln Asp Leu Lys Asp Gly
170 175 180
Thr Gln Glu Glu Ala Thr Lys Arg Gln Glu Ala Pro Val Asp Pro
185 190 195
Arg Pro Glu Gly Asp Pro Gln Arg Thr Val Ile Ser Trp Arg Gly
200 205 210
Ala Val Ile Glu Pro Glu Gln Gly Thr Glu Leu Pro Ser Arg Arg
215 220 225
Ala Glu Val Pro Thr Lys Pro Pro Leu Pro Pro Ala Arg Thr Gln
230 235 240
Gly Thr Pro Val His Leu Asn Tyr Arg Gln Lys Gly Val Ile Asp
245 250 255
Val Phe Leu His Ala Trp Lys Gly Tyr Arg Lys Phe Ala Trp Gly
260 265 270
His Asp Glu Leu Lys Pro Val Ser Arg Ser Phe Ser Glu Trp Phe
275 280 285
Gly Leu Gly Leu Thr Leu Ile Asp Ala Leu Asp Thr Met Trp Ile

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Leu	Gly	Leu	Arg	Lys	Glu	Phe	Glu	Glu	Ala	Arg	Lys	Trp	Val	Ser	
	305		310		315										
Lys	Lys	Leu	His	Phe	Glu	Lys	Asp	Val	Asp	Val	Asn	Leu	Phe	Glu	
	320		325		330										
Ser	Thr	Ile	Arg	Ile	Leu	Gly	Gly	Leu	Leu	Ser	Ala	Tyr	His	Leu	
	335		340		345										
Ser	Gly	Asp	Ser	Leu	Phe	Leu	Arg	Lys	Ala	Glu	Asp	Phe	Gly	Asn	
	350		355		360										
Arg	Leu	Met	Pro	Ala	Phe	Arg	Thr	Pro	Ser	Lys	Ile	Pro	Tyr	Ser	
	365		370		375										
Asp	Val	Asn	Ile	Gly	Thr	Gly	Val	Ala	His	Pro	Pro	Arg	Trp	Thr	
	380		385		390										
Ser	Asp	Ser	Thr	Val	Ala	Glu	Val	Thr	Ser	Ile	Gln	Leu	Glu	Phe	
	395		400		405										
Arg	Glu	Leu	Ser	Arg	Leu	Thr	Gly	Asp	Lys	Lys	Phe	Gln	Glu	Ala	
	410		415		420										
Val	Glu	Lys	Val	Thr	Gln	His	Ile	His	Gly	Leu	Ser	Gly	Lys	Lys	
	425		430		435										
Asp	Gly	Leu	Val	Pro	Met	Phe	Ile	Asn	Thr	His	Ser	Gly	Leu	Phe	
	440		445		450										
Thr	His	Leu	Gly	Val	Phe	Thr	Leu	Gly	Ala	Arg	Ala	Asp	Ser	Tyr	
	455		460		465										
Tyr	Glu	Tyr	Leu	Leu	Lys	Gln	Trp	Ile	Gln	Gly	Gly	Lys	Gln	Glu	
	470		475		480										
Thr	Gln	Leu	Leu	Glu	Asp	Tyr	Val	Glu	Ala	Ile	Glu	Gly	Val	Arg	
	485		490		495										
Thr	His	Leu	Leu	Arg	His	Ser	Glu	Pro	Ser	Lys	Leu	Thr	Phe	Val	
	500		505		510										
Gly	Glu	Leu	Ala	His	Gly	Arg	Phe	Ser	Ala	Lys	Met	Asp	His	Leu	
	515		520		525										
Val	Cys	Phe	Leu	Pro	Gly	Thr	Leu	Ala	Leu	Gly	Val	Tyr	His	Gly	
	530		535		540										
Leu	Pro	Ala	Ser	His	Met	Glu	Leu	Ala	Gln	Glu	Leu	Met	Glu	Thr	
	545		550		555										
Cys	Tyr	Gln	Met	Asn	Arg	Gln	Met	Glu	Thr	Gly	Leu	Ser	Pro	Glu	
	560		565		570										
Ile	Val	His	Phe	Asn	Leu	Tyr	Pro	Gln	Pro	Gly	Arg	Arg	Asp	Val	

	575	580	585
Glu Val Lys Pro Ala Asp Arg His Asn Leu Leu Arg Pro Glu Thr			
590	595	600	
Val Glu Ser Leu Phe Tyr Leu Tyr Arg Val Thr Gly Asp Arg Lys			
605	610	615	
Tyr Gln Asp Trp Gly Trp Glu Ile Leu Gln Ser Phe Ser Arg Phe			
620	625	630	
Thr Arg Val Pro Ser Gly Gly Tyr Ser Ser Ile Asn Asn Val Gln			
635	640	645	
Asp Pro Gln Lys Pro Glu Pro Arg Asp Lys Met Glu Ser Phe Phe			
650	655	660	
Leu Gly Glu Thr Leu Lys Tyr Leu Phe Leu Leu Phe Ser Asp Asp			
665	670	675	
Pro Asn Leu Leu Ser Leu Asp Ala Tyr Val Phe Asn Thr Glu Ala			
680	685	690	
His Pro Leu Pro Ile Trp Thr Pro Ala			
695			

<210> 13

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 13

cggcagaagg gcgtgattga cgtc 24

<210> 14

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 14

ccatccttct tcccagacag gccg 24

<210> 15

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 15

gaagcctgtg tccaggtcct tcagttagtg gtttggcctc ggtc 44
<210> 16
<211> 1524
<212> DNA
<213> Homo sapiens .

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ccctcggaag tgttccgtct tccacctgtt cgtggcctgc ctctcgctgg 200
gcttcttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250
cggcagtcg ggggacaagg gcaggagacc tcggggccctc cccgtgcctg 300
ccccccagag ccgccccctg agcactggga agaagacgca tcctggggcc 350
cccacccgcct ggcagtgctg gtgccttcc gcgaacgctt cgaggagctc 400
ctggtcttcg tgccccacat gcgcgccttc ctgagcagga agaagatccg 450
gcaccacatc tacgtgctca accaggtgga ccacttcagg ttcaaccggg 500
cagcgctcat caacgtggc ttccctggaga gcagcaacag cacggactac 550
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cagcactacc ggctgtgcaa tggatgtcc aaccgcttct gggctgggg 750
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aaaaaaaaaa aaaaaaaaaa aaaa 1524

<210> 17
<211> 327
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-42
<223> Signal peptide.

<220>
<221> misc_feature
<222> 19-25,65-71,247-253,285-291,303-310
<223> N-myristoylation site.

<220>
<221> misc_feature
<222> 27-31
<223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>
<221> TRANSMEM
<222> 29-49
<223> Transmembrane domain (type II).

<220>
<221> misc_feature
<222> 154-158
<223> N-glycosylation site.

<220>
<221> misc_feature
<222> 226-233
<223> Tyrosine kinase phosphorylation site.

<400> 17
Met Phe Pro Ser Arg Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp
1 5 10 15

Gly Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser
20 25 30

Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser
35 40 45

Leu Leu Trp Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala
50 55 60

Val Arg Gly Gln Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys
65 70 75

Pro Pro Glu Pro Pro Glu His Trp Glu Glu Asp Ala Ser Trp
80 85 90

Gly Pro His Arg Leu Ala Val Leu Val Pro Phe Arg Glu Arg Phe
95 100 105

Glu Glu Leu Leu Val Phe Val Pro His Met Arg Arg Phe Leu Ser
110 115 120

Arg Lys Lys Ile Arg His His Ile Tyr Val Leu Asn Gln Val Asp
125 130 135

His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu
140 145 150

Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala Met His Asp Val Asp
155 160 165

Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly Phe Pro Glu Ala
170 175 180

Gly Pro Phe His Val Ala Ser Pro Glu Leu His Pro Leu Tyr His
185 190 195

Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys Gln His
200 205 210

Tyr Arg Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp Gly
215 220 225

Arg Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu
230 235 240

Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Lys Thr Phe
245 250 255

Arg His Leu His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg
260 265 270

Ile Ala Ala Gln Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly
275 280 285

Gly Leu Asn Thr Val Lys Tyr His Val Ala Ser Arg Thr Ala Leu
290 295 300

Ser Val Gly Gly Ala Pro Cys Thr Val Leu Asn Ile Met Leu Asp
305 310 315

Cys Asp Lys Thr Ala Thr Pro Trp Cys Thr Phe Ser
320 325

<210> 18
<211> 23
<212> DNA
<> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 18
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<210> 19
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 19
gcagtgcggg aagccacatg gtac 24

<210> 20
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 20
cttcctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21
<211> 494
<212> DNA
<213> Homo sapiens

<400> 21
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gactggtcgg tgcccagaaa gtctcttctg ccactgacgc ccccatcagg 150
gattgggcct tcttcccccc ttcccttctg tgtctcctgc ctcatacgcc 200
tgccatgacc tgcatgcaag cccagccccg tggggaaagg gaaaaagtgg 250
ggatggcta agaaagctgg gagataggga acagaagagg gtagtgggtg 300
ggcttaggggg gctgccttat ttaaagtgg tggatgtat tcttatacta 350
atttatacaa agatattaag gccctgttca ttaagaaatt gttcccttcc 400
cctgtgttca atgtttgtaa agattgttct gtgtaaatat gtctttataa 450

taaacagtta aaagctgaaa aaaaaaaaaaa aaaaaaaaaaa aaaa 494

<210> 22

<211> 73

<212> PRT

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 1-15

<223> Signal peptide.

<220>

<221> misc_feature

<222> 3-18

<223> Growth factor and cytokines receptors family.

<400> 22

Met Leu Leu Leu Thr Leu Leu Leu Leu Leu Leu Lys Gly
1 5 10 15

Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser
20 25 30

Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser
35 40 45

Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln
50 55 60

Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly
65 70

<210> 23

<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

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ccataaggct ccggtcgccc ctgggccccgc gccgcgtcc tgcccggccg 150

ggctccgggg cggccccta ggccagtgcg ccgcgcgtcg ccccgcaggc 200

cccgccccgc agcatggagc cacccggacg cggcgggggc cgcgcgcaagc 250

cgcgcgtgtt gctgccgctc tcgctgttag cgctgctcgc gctgctggga 300

ggcggcggcg gcggcgccgc cgccggcgctg cccgcggct gcaagcacga 350

tggcgccccc cgaggggctg gcagggcgcc gggcgccgccc gagggcaagg 400

tggtgtcag cagcctggaa ctgcgcgagg tcctgcccc agatactctg 450

cccaaccgca cggtcaccct gattctgagt aacaataaga tatccgagct 500
gaagaatggc tcattttctg ggttaagtct ccttcaaaga ttggacctcc 550
gaaacaatct tatttagtagt atagatccag gtgccttctg gggactgtca 600
tctctaaaaa gattggatct gacaaacaat cgaataggat gtctgaatgc 650
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atttgaaaa ttcattatct caaggaacct ttgattatct tgcgtcatta 750
cggtcttgg aattccagac tgagtatctt ttgtgtgact gtaacatact 800
gtggatgcat cgctggtaa aggagaagaa catcacgta cgggatacca 850
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gactccatct catgccaag ttgtgttga aggagacagc cttcccttcc 1000
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gatgggagaa tagtgaaac cgatgaatcg caaggatatt ttgttgaaaa 1100
gaacatgatt cacaactgct cttgattgc aagtgccta accatttcta 1150
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<213> Homo sapiens

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<222> 1-33
<223> Signal peptide.

<220>
<221> TRANSMEM
<222> 13-40
<223> Transmembrane domain (type II).

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Asp	Gly	Arg	Pro	Arg	Gly	Ala	Gly	Arg	Ala	Ala	Gly	Ala	Ala
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Gly	Lys	Val	Val	Cys	Ser	Ser	Leu	Glu	Leu	Ala	Gln	Val	Leu
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Pro	Asp	Thr	Leu	Pro	Asn	Arg	Thr	Val	Thr	Leu	Ile	Leu	Ser
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Asn	Lys	Ile	Ser	Glu	Leu	Lys	Asn	Gly	Ser	Phe	Ser	Gly	Leu
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Leu	Leu	Glu	Arg	Leu	Asp	Leu	Arg	Asn	Asn	Leu	Ile	Ser	Ser
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Asp	Pro	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Ser	Leu	Lys	Arg	Leu
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Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe
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Ser	Ser	Leu	Ser	Gln	Gly	Thr	Phe	Asp	Tyr	Leu	Ala	Ser	Leu
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Ser	Leu	Glu	Phe	Gln	Thr	Glu	Tyr	Leu	Leu	Cys	Asp	Cys	Asn
				185					190				195
Leu	Trp	Met	His	Arg	Trp	Val	Lys	Glu	Lys	Asn	Ile	Thr	Val
				200					205				210
Asp	Thr	Arg	Cys	Val	Tyr	Pro	Lys	Ser	Leu	Gln	Ala	Gln	Pro
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Thr	Gly	Val	Lys	Gln	Glu	Leu	Leu	Thr	Cys	Asp	Pro	Pro	Leu
				230					235				240
Leu	Pro	Ser	Phe	Tyr	Met	Thr	Pro	Ser	His	Arg	Gln	Val	Val
				245					250				255
Glu	Gly	Asp	Ser	Leu	Pro	Phe	Gln	Cys	Met	Ala	Ser	Tyr	Ile
				260					265				270
Gln	Asp	Met	Gln	Val	Leu	Trp	Tyr	Gln	Asp	Gly	Arg	Ile	Val
				275					280				285

Thr Asp Glu Ser Gln Gly Ile Phe Val Glu Lys Asn Met Ile His
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Asn Cys Ser Leu Ile Ala Ser Ala Leu Thr Ile Ser Asn Ile Gln
305 310 315

Ala Gly Ser Thr Gly Asn Trp Gly Cys His Val Gln Thr Lys Arg
320 325 330

Gly Asn Asn Thr Arg Thr Val Asp Ile Val Val Leu Glu Ser Ser
335 340 345

Ala Gln Tyr Cys Pro Pro Glu Arg Val Val Asn Asn Lys Gly Asp
350 355 360

Phe Arg Trp Pro Arg Thr Leu Ala Gly Ile Thr Ala Tyr Leu Gln
365 370 375

Cys Thr Arg Asn Thr His Gly Ser Gly Ile Tyr Pro Gly Asn Pro
380 385 390

Gln Asp Glu Arg Lys Ala Trp Arg Arg Cys Asp Arg Gly Gly Phe
395 400 405

Trp Ala Asp Asp Asp Tyr Ser Arg Cys Gln Tyr Ala Asn Asp Val
410 415 420

Thr Arg Val Leu Tyr Met Phe Asn Gln Met Pro Leu Asn Leu Thr
425 430 435

Asn Ala Val Ala Thr Ala Arg Gln Leu Leu Ala Tyr Thr Val Glu
440 445 450

Ala Ala Asn Phe Ser Asp Lys Met Asp Val Ile Phe Val Ala Glu
455 460 465

Met Ile Glu Lys Phe Gly Arg Phe Thr Lys Glu Glu Lys Ser Lys
470 475 480

Glu Leu Gly Asp Val Met Val Asp Ile Ala Ser Asn Ile Met Leu
485 490 495

Ala Asp Glu Arg Val Leu Trp Leu Ala Gln Arg Glu Ala Lys Ala
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Cys Ser Arg Ile Val Gln Cys Leu Gln Arg Ile Ala Thr Tyr Arg
515 520 525

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Ala Leu Glu Ala Tyr Val Ile Lys Ser Thr Gly Phe Thr Gly Met
545 550 555

Thr Cys Thr Val Phe Gln Lys Val Ala Ala Ser Asp Arg Thr Gly
560 565 570

Leu Ser Asp Tyr Gly Arg Arg Asp Pro Glu Gly Asn Leu Asp Lys
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Ala Leu Lys Val Cys Tyr Ile Leu Gln Ser Phe Lys Thr Ile Tyr
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Ser

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<212> DNA
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 26
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 26
aactggaaaag gaaggctgtc tccc 24

<210> 27
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
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<211> 683
<212> DNA
<213> Homo sapiens

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gcagaggctt cgtgaçggag ttatcagaga cattgagagg caaattcgga 150

aaaaagaaaa cattcgctt ttgggagaac agattatttt gactgagcaa 200
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<211> 81
<212> PRT
<213> Homo sapiens

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<222> 1-21
<223> Signal peptide.

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Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln
35 40 45
Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile
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65 70 75
Lys Gly Ser Gln Lys Ser
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<212> DNA
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<211> 322
<212> PRT
<213> Homo sapiens

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35 40 45
Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp
50 55 60
Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys
65 70 75
Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu
80 85 90
Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe
95 100 105

Ala	Cys	Tyr	Ala	Ala	Leu	Phe	Cys	Leu	Ser	Ala	Ser	Ile	Ile	Tyr
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Pro	Thr	Thr	Tyr	Val	Gln	Phe	Leu	Ser	His	Gly	Arg	Ser	Arg	Asp
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125														
His	Ala	Ile	Ala	Ala	Thr	Phe	Phe	Ser	Cys	Ile	Ala	Cys	Val	Ala
									145					150
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Tyr	Ala	Thr	Glu	Val	Ala	Trp	Thr	Arg	Ala	Arg	Pro	Gly	Glu	Ile
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155														
Thr	Gly	Tyr	Met	Ala	Thr	Val	Pro	Gly	Leu	Leu	Lys	Val	Leu	Glu
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170														
Thr	Phe	Val	Ala	Cys	Ile	Ile	Phe	Ala	Phe	Ile	Ser	Asp	Pro	Asn
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									205					210
200														
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215														
Gly	Glu	Cys	Thr	Asn	Val	Leu	Pro	Ile	Pro	Phe	Pro	Ser	Phe	Leu
									235					240
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Ser	Gly	Leu	Ala	Leu	Leu	Ser	Val	Leu	Leu	Tyr	Ala	Thr	Ala	Leu
									250					255
245														
Val	Leu	Trp	Pro	Leu	Tyr	Gln	Phe	Asp	Glu	Lys	Tyr	Gly	Gly	Gln
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Pro	Arg	Arg	Ser	Arg	Asp	Val	Ser	Cys	Ser	Arg	Ser	His	Ala	Tyr
									280					285
275														
Tyr	Val	Cys	Ala	Trp	Asp	Arg	Arg	Leu	Ala	Val	Ala	Ile	Leu	Thr
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290														
Ala	Ile	Asn	Leu	Leu	Ala	Tyr	Val	Ala	Asp	Leu	Val	His	Ser	Ala
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<210> 32

<211> 3680

<212> DNA

<213> Homo sapiens

<400> 32

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<210> 33

<211> 335

<212> PRT

<213> Homo sapiens

<400> 33

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Phe	Gly	Thr	Val	Ser	Cys	Glu	Tyr	Met	Leu	Gly	Ser	Pro	Leu	Ser
					20				25				30	

Ser	Leu	Ala	Gln	Val	Asn	Leu	Ser	Pro	Phe	Ser	His	Pro	Lys	Val
					35				40				45	

His	Met	Asp	Pro	Asn	Tyr	Cys	His	Pro	Ser	Thr	Ser	Leu	His	Leu
							50		55				60	

Cys	Ser	Leu	Ala	Trp	Ser	Phe	Thr	Arg	Leu	Leu	His	Pro	Pro	Leu
						65			70				75	

Ser	Pro	Gly	Ile	Ser	Gln	Val	Val	Lys	Asp	His	Val	Thr	Lys	Pro
						80			85				90	

Thr	Ala	Met	Ala	Gln	Gly	Arg	Val	Ala	His	Leu	Ile	Glu	Trp	Lys
							95			100			105	

Gly	Trp	Ser	Lys	Pro	Ser	Asp	Ser	Pro	Ala	Ala	Leu	Glu	Ser	Ala
								110		115			120	

Phe Ser Ser Tyr Ser Asp Leu Ser Glu Gly Glu Gln Glu Ala Arg
125 130 135

Phe Ala Ala Gly Val Ala Glu Gln Phe Ala Ile Ala Glu Ala Lys
140 145 150

Leu Arg Ala Trp Ser Ser Val Asp Gly Glu Asp Ser Thr Asp Asp
155 160 165

Ser Tyr Asp Glu Asp Phe Ala Gly Gly Met Asp Thr Asp Met Ala
170 175 180

Gly Gln Leu Pro Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly
185 190 195

His Arg Phe Ser Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu
200 205 210

Ser Asp Cys Ser Gln Thr Val Ser Pro Asp Thr Leu Cys Ser Ser
215 220 225

Leu Cys Ser Leu Glu Asp Gly Leu Leu Gly Ser Pro Ala Arg Leu
230 235 240

Ala Ser Gln Leu Leu Gly Asp Glu Leu Leu Leu Ala Lys Leu Pro
245 250 255

Pro Ser Arg Glu Ser Ala Phe Arg Ser Leu Gly Pro Leu Glu Ala
260 265 270

Gln Asp Ser Leu Tyr Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser
275 280 285

Pro Ala Glu Glu Glu Pro Ala Pro Cys Lys Asp Cys Gln Pro Leu
290 295 300

Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg Gln Arg Gln Ala Ser
305 310 315

Asp Leu Ala Ser Ser Gly Val Val Ser Leu Asp Glu Asp Glu Ala
320 325 330

Glu Pro Glu Glu Gln
335

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<211> 25
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<220>
<223> Synthetic oligonucleotide probe

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tgtccttgc cccagacttc tgtcc 25

<210> 35
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
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<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 36
ttccactcaa tgaggtgagc cactc 25

<210> 37
<211> 23
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 37
ggcgagccct aactatccag gag 23

<210> 38
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 38
ggagatcgct gcgctggcca ggtcctccct gcatggtat 39

<210> 39
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 39
ctgctgcaaa gcgagcctct tg 22

<210> 40
<211> 2084

<212> DNA
<213> Homo sapiens

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ccatctgttt tctctaattgc acgacagatt ccttcagac aggacaactg 150
tgatatttca gttcctgatt gtaataacct cctaaggctg aagcttctgt 200
tactagccat tgtgagcttc agtttcttca tctgcaaaat gggcataata 250
caatctattc ttgccacatc aaggattgt tattcctta aaaaaaaacc 300
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caacgttggtt ttattcactt ctatcgaaaa ggcattggaaa agaaaaatcaa 400
gacataaaaca caacacagaa cattgcagaa gttttaaaaa caatggaaaa 450
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ttgggtgcct taaaaactca atgagaatca tggt 2084

<210> 41
<211> 334
<212> PRT
<213> Homo sapiens

<400> 41
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Ser Leu Leu Ser Gly Ser His Gly Lys Glu Asn Gln Asp Ile Asn
20 25 30
Thr Thr Gln Asn Ile Ala Glu Val Phe Lys Thr Met Glu Asn Lys
35 40 45
Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu
50 55 60
Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu
65 70 75
Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn
80 85 90
Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr
95 100 105

Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val
110 115 120

Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser
125 130 135

Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr
140 145 150

Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser
155 160 165

Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val
170 175 180

Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser
185 190 195

Asp Ser Phe Thr Gly Phe Thr Pro Tyr Gln Glu Lys Thr Thr Leu
200 205 210

Gln Pro Thr Leu Lys Phe Thr Asn Asn Ser Lys Leu Phe Pro Asn
215 220 225

Thr Ser Asp Pro Gln Lys Glu Asn Arg Asn Thr Gly Ile Val Phe
230 235 240

Gly Ala Ile Leu Gly Ala Ile Leu Gly Val Ser Leu Leu Thr Leu
245 250 255

Val Gly Tyr Leu Leu Cys Gly Lys Arg Lys Thr Asp Ser Phe Ser
260 265 270

His Arg Arg Leu Tyr Asp Asp Arg Asn Glu Pro Val Leu Arg Leu
275 280 285

Asp Asn Ala Pro Glu Pro Tyr Asp Val Ser Phe Gly Asn Ser Ser
290 295 300

Tyr Tyr Asn Pro Thr Leu Asn Asp Ser Ala Met Pro Glu Ser Glu
305 310 315

Glu Asn Ala Arg Asp Gly Ile Pro Met Asp Asp Ile Pro Pro Leu
320 325 330

Arg Thr Ser Val

<210> 42
<211> 1594
<212> DNA
<213> Homo sapiens

<400> 42
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ccccctaccgc cgtgcaaaag gaggaggcgc ggcaagacgt ggaggccctc 150
ctgagccgca cggtcagaac tcagatactg accggcaagg agctccgagt 200
tgccaccagg gaaaaagagg gtcctctgg gagatgtatg cttaactct 250
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tacaagtact tcatgcccga gagcaccatt taccgtggag agatgtgctt 350
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ccctataata aattttactc tatacaaaaa aaaaaaaaaaaa aaaa 1594

<210> 43
<211> 263
<212> PRT
<213> Homo sapiens

<400> 43

Met	Val	Lys	Ile	Ala	Phe	Asn	Thr	Pro	Thr	Ala	Val	Gln	Lys	Glu
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Glu Ala Arg Gln Asp Val Glu Ala Leu Leu Ser Arg Thr Val Arg

	20									25				30
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Thr Gln Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu

		35							40					45
--	--	----	--	--	--	--	--	--	----	--	--	--	--	----

Lys Glu Gly Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu

		50						55						60
--	--	----	--	--	--	--	--	----	--	--	--	--	--	----

Ser Phe Ile Leu Ala Gly Leu Ile Val Gly Gly Ala Cys Ile Tyr

		65					70							75
--	--	----	--	--	--	--	----	--	--	--	--	--	--	----

Lys Tyr Phe Met Pro Lys Ser Thr Ile Tyr Arg Gly Glu Met Cys

		80					85							90
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Phe Phe Asp Ser Glu Asp Pro Ala Asn Ser Leu Arg Gly Gly Glu

		95					100							105
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Pro Asn Phe Leu Pro Val Thr Glu Glu Ala Asp Ile Arg Glu Asp

		110					115							120
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Asp Asn Ile Ala Ile Ile Asp Val Pro Val Pro Ser Phe Ser Asp

		125					130							135
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Ser Asp Pro Ala Ala Ile Ile His Asp Phe Glu Lys Gly Met Thr

		140					145							150
--	--	-----	--	--	--	--	-----	--	--	--	--	--	--	-----

Ala Tyr Leu Asp Leu Leu Leu Gly Asn Cys Tyr Leu Met Pro Leu

		155					160							165
--	--	-----	--	--	--	--	-----	--	--	--	--	--	--	-----

Asn Thr Ser Ile Val Met Pro Pro Lys Asn Leu Val Glu Leu Phe

		170					175							180
--	--	-----	--	--	--	--	-----	--	--	--	--	--	--	-----

Gly Lys Leu Ala Ser Gly Arg Tyr Leu Pro Gln Thr Tyr Val Val

		185					190							195
--	--	-----	--	--	--	--	-----	--	--	--	--	--	--	-----

Arg Glu Asp Leu Val Ala Val Glu Glu Ile Arg Asp Val Ser Asn

		200					205							210
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Leu Gly Ile Phe Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser Phe

		215					220							225
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Arg Leu Arg Arg Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala

230 235 240

Ile Asp Lys Cys Trp Lys Ile Arg His Phe Pro Asn Glu Phe Ile
245 250 255

Val Glu Thr Lys Ile Cys Gln Glu
260

<210> 44
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 44
gaaagacacg acacagcagc ttgc 24

<210> 45
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 45
ggaaactgct atctgatgcc 20

<210> 46
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 46
caggatctcc tcttgagtc tgca 26

<210> 47
<211> 28
<212> DNA
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<220>
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<400> 47
cttctcgAAC cacataagtt tgaggcag 28

<210> 48
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 48
cacgattccc tccacagcaa ctggg 25

<210> 49
<211> 1969
<212> DNA
<213> Homo sapiens

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ggaggaggga gggcgggcag ggcgcagccc agagcagccc cgggcaccag 50
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gtttcggcgg cagccccag ctcctcatac cttctgttgc tgctgctggg 200
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ggcaggaggt cctctcccc atccctccat ctgggctcc cccaacctct 1850
gcacagctct ccaggtgctg agatataatg caccagcaca ataaaccttt 1900
attccggcct gaaaaaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa 1950
aaaaaaaaaaa aaaaaaaaaga 1969

<210> 50
<211> 283
<212> PRT
<213> Homo sapiens

<400> 50
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20 25 30

Lys Ala Thr Phe Leu Glu Asp Val Ala Gly Ser Gly Glu Ala Glu
35 40 45

Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro
50 55 60

Ala Leu Ser Pro Thr Ser Met Gly Pro Gln Pro Thr Thr Leu Gly
65 70 75

Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe

80	85	90
Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val Gly Ser Leu Ala		
95	100	105
Phe Leu Leu Met Phe Ile Val Cys Ala Ala Val Ile Thr Arg Gln		
110	115	120
Lys Gln Lys Ala Ser Ala Tyr Tyr Pro Ser Ser Phe Pro Lys Lys		
125	130	135
Lys Tyr Val Asp Gln Ser Asp Arg Ala Gly Gly Pro Arg Ala Phe		
140	145	150
Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Pro Glu Glu Ala		
155	160	165
Leu Asp Ser Ser Arg Gln Leu Gln Ala Asp Ile Leu Ala Ala Thr		
170	175	180
Gln Asn Leu Lys Ser Pro Thr Arg Ala Ala Leu Gly Gly Asp		
185	190	195
Gly Ala Arg Met Val Glu Gly Arg Gly Ala Glu Glu Glu Lys		
200	205	210
Gly Ser Gln Glu Gly Asp Gln Glu Val Gln Gly His Gly Val Pro		
215	220	225
Val Glu Thr Pro Glu Ala Gln Glu Glu Pro Cys Ser Gly Val Leu		
230	235	240
Glu Gly Ala Val Val Ala Gly Glu Gly Gln Gly Glu Leu Glu Gly		
245	250	255
Ser Leu Leu Leu Ala Gln Glu Ala Gln Gly Pro Val Gly Pro Pro		
260	265	270
Glu Ser Pro Cys Ala Cys Ser Ser Val His Pro Ser Val		
275	280	

<210> 51
 <211> 1734
 <212> DNA
 <213> Homo sapiens

<400> 51
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 agacactctg gagagagagg gggctggca gagatgaagt tccagggcc 200
 cctggcctgc ctcctgctgg ccctctgcct gggcagtggg gaggctggcc 250

ccctgcagag cgagaggaa agcactggg caaatattgg ggaggccctt 300
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caaagaggcc ggagggcag ctggctctaa agtcagttag gcccttgcc 400
aagggaccag agaagcagtt ggcactggag tcaggcaggt tccaggctt 450
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acggagcaga tgctgtccgc ggctcctggc aggggtgcc tggccacagt 600
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1700

aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaa 1734

<210> 52

<211> 440

<212> PRT

<213> Homo sapiens

<400> 52

Met Lys Phe Gln Gly Pro Leu Ala Cys Leu Leu Leu Ala Leu Cys
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Leu Gly Ser Gly Glu Ala Gly Pro Leu Gln Ser Gly Glu Glu Ser
20 25 30

Thr Gly Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp
35 40 45

Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly
50 55 60

Gly Ala Ala Gly Ser Lys Val Ser Glu Ala Leu Gly Gln Gly Thr
65 70 75

Arg Glu Ala Val Gly Thr Gly Val Arg Gln Val Pro Gly Phe Gly
80 85 90

Ala Ala Asp Ala Leu Gly Asn Arg Val Gly Glu Ala Ala His Ala
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Leu Gly Asn Thr Gly His Glu Ile Gly Arg Gln Ala Glu Asp Val
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Ile Arg His Gly Ala Asp Ala Val Arg Gly Ser Trp Gln Gly Val
125 130 135

Pro Gly His Ser Gly Ala Trp Glu Thr Ser Gly Gly His Gly Ile
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Phe Gly Ser Gln Gly Gly Leu Gly Gly Gln Gly Gln Gly Asn Pro
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Gly Gly Leu Gly Thr Pro Trp Val His Gly Tyr Pro Gly Asn Ser
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Ala Gly Ser Phe Gly Met Asn Pro Gln Gly Ala Pro Trp Gly Gln
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Gly Gly Asn Gly Gly Pro Pro Asn Phe Gly Thr Asn Thr Gln Gly
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Ala Val Ala Gln Pro Gly Tyr Gly Ser Val Arg Ala Ser Asn Gln
215 220 225

Asn Glu Gly Cys Thr Asn Pro Pro Pro Ser Gly Ser Gly Gly Gly
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Ser Ser Asn Ser Gly Gly Ser Gly Ser Gln Ser Gly Ser Ser
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 Gly Ser Ser Ser Gly Ser Ser Ser Gly Ser Ser Ser Gly Gly Ser
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 Glu Ser Gly Ile Gln Gly Phe Arg Gly Gln Gly Val Ser Ser Asn
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 Met Arg Glu Ile Ser Lys Glu Gly Asn Arg Leu Leu Gly Gly Ser
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 Gly Asp Asn Tyr Arg Gly Gln Gly Ser Ser Trp Gly Ser Gly Gly
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 Gly Asp Ala Val Gly Gly Val Asn Thr Val Asn Ser Glu Thr Ser
 395 400 405
 Pro Gly Met Phe Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys Ser
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<400> 54
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Glu Gly Pro Ser Tyr Ala Phe Glu Val Asp Thr Val Ala Pro Glu
35 40 45

His Gly Leu Asp Asn Ala Pro Val Val Asp Gln Gln Leu Leu Tyr
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Thr Cys Cys Pro Tyr Ile Gly Glu Leu Arg Lys Leu Leu Ala Ser
65 70 75

Trp Val Ser Gly Ser Ser Gly Arg Ser Gly Gly Phe Met Arg Lys
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Ile Thr Pro Thr Thr Ser Leu Gly Ala Gln Pro Ser Gln
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Thr Ser Gln Gly Leu Gln Ala Gln Leu Ala Gln Ala Phe Phe His
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Asn Gln Pro Pro Ser Leu Arg Arg Thr Val Glu Phe Val Ala Glu
125 130 135

Arg Ile Gly Ser Asn Cys Val Lys His Ile Lys Ala Thr Leu Val
140 145 150

Ala Asp Leu Val Arg Gln Ala Glu Ser Leu Leu Gln Glu Gln Leu
155 160 165

Val Thr Gln Gly Glu Glu Gly Gly Asp Pro Ala Gln Leu Leu Glu
170 175 180

Ile Leu Cys Ser Gln Leu Cys Pro His Gly Ala Gln Ala Leu Ala
185 190 195

Leu Gly Arg Glu Phe Cys Gln Arg Lys Ser Pro Gly Ala Val Arg
200 205 210

Ala Leu Leu Pro Glu Glu Thr Pro Ala Ala Val Leu Ser Ser Ala
215 220 225

Glu Asn Ile Ala Val Gly Leu Ala Thr Glu Lys Ala Cys Ala Trp
230 235 240

Leu Ser Ala Asn Ile Thr Ala Leu Ile Arg Arg Glu Val Lys Ala
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Pro Val Asn Leu Lys Lys Trp Ser Ile Thr Asp Gly Tyr Val Pro
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Ile Leu Gly Asn Lys Thr Leu Pro Ser Arg Cys His Gln Cys Val
65 70 75
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Glu Ile Glu Arg Ala Glu Cys Thr Ile Arg Met Asn Asp Ala Pro
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Thr Thr Gly Tyr Ser Ala Asp Val Gly Asn Lys Thr Thr Tyr Arg
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Val Val Ala His Ser Ser Val Phe Arg Val Leu Arg Arg Pro Gln
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Glu Phe Val Asn Arg Thr Pro Glu Thr Val Phe Ile Phe Trp Gly
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Pro Pro Ser Lys Met Gln Lys Pro Gln Gly Ser Leu Val Arg Val
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Ile Gln Arg Ala Gly Leu Val Phe Pro Asn Met Glu Ala Tyr Ala

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Glu Thr Gly Lys Asp Arg Glu Lys Ser His Ser Trp Leu Ser Thr			
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Gly Trp Phe Thr Met Val Ile Ala Val Glu Leu Cys Asp His Val			
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His Val Tyr Gly Met Val Pro Pro Asn Tyr Cys Ser Gln Arg Pro			
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Arg Leu Gln Arg Met Pro Tyr His Tyr Tyr Glu Pro Lys Gly Pro			
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Asp Glu Cys Val Thr Tyr Ile Gln Asn Glu His Ser Arg Lys Gly			
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<212> PRT
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<400> 58
Met Leu Arg Gly Thr Met Thr Ala Trp Arg Gly Met Arg Pro Glu
1 5 10 15

Val Thr Leu Ala Cys Leu Leu Leu Ala Thr Ala Gly Cys Phe Ala
20 25 30

Asp Leu Asn Glu Val Pro Gln Val Thr Val Gln Pro Ala Ser Thr
35 40 45

Val Gln Lys Pro Gly Gly Thr Val Ile Leu Gly Cys Val Val Glu
50 55 60

Pro Pro Arg Met Asn Val Thr Trp Arg Leu Asn Gly Lys Glu Leu
65 70 75

Asn Gly Ser Asp Asp Ala Leu Gly Val Leu Ile Thr His Gly Thr
80 85 90

Leu Val Ile Thr Ala Leu Asn Asn His Thr Val Gly Arg Tyr Gln
95 100 105

Cys Val Ala Arg Met Pro Ala Gly Ala Val Ala Ser Val Pro Ala
110 115 120

Thr Val Thr Leu Ala Asn Leu Gln Asp Phe Lys Leu Asp Val Gln
125 130 135

His Val Ile Glu Val Asp Glu Gly Asn Thr Ala Val Ile Ala Cys
140 145 150

His Leu Pro Glu Ser His Pro Lys Ala Gln Val Arg Tyr Ser Val
155 160 165

Lys Gln Glu Trp Leu Glu Ala Ser Arg Gly Asn Tyr Leu Ile Met
170 175 180

Pro Ser Gly Asn Leu Gln Ile Val Asn Ala Ser Gln Glu Asp Glu
185 190 195

Gly Met Tyr Lys Cys Ala Ala Tyr Asn Pro Val Thr Gln Glu Val
200 205 210

Lys Thr Ser Gly Ser Ser Asp Arg Leu Arg Val Arg Arg Ser Thr
215 220 225

Ala Glu Ala Ala Arg Ile Ile Tyr Pro Pro Glu Ala Gln Thr Ile
230 235 240

Ile Val Thr Lys Gly Gln Ser Leu Ile Leu Glu Cys Val Ala Ser
245 250 255

Gly Ile Pro Pro Pro Arg Val Thr Trp Ala Lys Asp Gly Ser Ser
260 265 270

Val Thr Gly Tyr Asn Lys Thr Arg Phe Leu Leu Ser Asn Leu Leu
275 280 285

Ile Asp Thr Thr Ser Glu Glu Asp Ser Gly Thr Tyr Arg Cys Met
290 295 300

Ala Asp Asn Gly Val Gly Gln Pro Gly Ala Ala Val Ile Leu Tyr
305 310 315

Asn Val Gln Val Phe Glu Pro Pro Glu Val Thr Met Glu Leu Ser
320 325 330

Gln Leu Val Ile Pro Trp Gly Gln Ser Ala Lys Leu Thr Cys Glu
335 340 345

Val Arg Gly Asn Pro Pro Pro Ser Val Leu Trp Leu Arg Asn Ala
350 355 360

Val Pro Leu Ile Ser Ser Gln Arg Leu Arg Leu Ser Arg Arg Ala
365 370 375

Leu Arg Val Leu Ser Met Gly Pro Glu Asp Glu Gly Val Tyr Gln
380 385 390

Cys Met Ala Glu Asn Glu Val Gly Ser Ala His Ala Val Val Gln
395 400 405

Leu Arg Thr Ser Arg Pro Ser Ile Thr Pro Arg Leu Trp Gln Asp
410 415 420

Ala Glu Leu Ala Thr Gly Thr Pro Pro Val Ser Pro Ser Lys Leu
425 430 435

Gly Asn Pro Glu Gln Met Leu Arg Gly Gln Pro Ala Leu Pro Arg
440 445 450

Pro Pro Thr Ser Val Gly Pro Ala Ser Pro Lys Cys Pro Gly Glu
455 460 465

Lys Gly Gln Gly Ala Pro Ala Glu Ala Pro Ile Ile Leu Ser Ser
470 475 480

Pro Arg Thr Ser Lys Thr Asp Ser Tyr Glu Leu Val Trp Arg Pro
485 490 495

Arg His Glu Gly Ser Gly Arg Ala Pro Ile Leu Tyr Tyr Val Val
500 505 510

Lys His Arg Lys Gln Val Thr Asn Ser Ser Asp Asp Trp Thr Ile
515 520 525

Ser Gly Ile Pro Ala Asn Gln His Arg Leu Thr Leu Thr Arg Leu
530 535 540

Asp Pro Gly Ser Leu Tyr Glu Val Glu Met Ala Ala Tyr Asn Cys
545 550 555

Ala Gly Glu Gly Gln Thr Ala Met Val Thr Phe Arg Thr Gly Arg
560 565 570

Arg Pro Lys Pro Glu Ile Met Ala Ser Lys Glu Gln Gln Ile Gln
575 580 585

Arg Asp Asp Pro Gly Ala Ser Pro Gln Ser Ser Ser Gln Pro Asp
590 595 600

His Gly Arg Leu Ser Pro Pro Glu Ala Pro Asp Arg Pro Thr Ile
605 610 615

Ser Thr Ala Ser Glu Thr Ser Val Tyr Val Thr Trp Ile Pro Arg
620 625 630

Gly Asn Gly Gly Phe Pro Ile Gln Ser Phe Arg Val Glu Tyr Lys
635 640 645

Lys Leu Lys Lys Val Gly Asp Trp Ile Leu Ala Thr Ser Ala Ile
650 655 660

Pro Pro Ser Arg Leu Ser Val Glu Ile Thr Gly Leu Glu Lys Gly
665 670 675

Thr Ser Tyr Lys Phe Arg Val Arg Ala Leu Asn Met Leu Gly Glu
680 685 690

Ser Glu Pro Ser Ala Pro Ser Arg Pro Tyr Val Val Ser Gly Tyr
695 700 705

Ser Gly Arg Val Tyr Glu Arg Pro Val Ala Gly Pro Tyr Ile Thr
710 715 720

Phe Thr Asp Ala Val Asn Glu Thr Thr Ile Met Leu Lys Trp Met
725 730 735

Tyr Ile Pro Ala Ser Asn Asn Asn Thr Pro Ile His Gly Phe Tyr
740 745 750

Ile Tyr Tyr Arg Pro Thr Asp Ser Asp Asn Asp Ser Asp Tyr Lys
755 760 765

Lys Asp Met Val Glu Gly Asp Lys Tyr Trp His Ser Ile Ser His
770 775 780

Leu Gln Pro Glu Thr Ser Tyr Asp Ile Lys Met Gln Cys Phe Asn
785 790 795

Glu Gly Gly Ser Glu Phe Ser Asn Val Met Ile Cys Glu Thr
800 805 810

Lys Ala Arg Lys Ser Ser Gly Gln Pro Gly Arg Leu Pro Pro Pro
815 820 825

Thr Leu Ala Pro Pro Gln Pro Pro Leu Pro Glu Thr Ile Glu Arg
830 835 840

Pro Val Gly Thr Gly Ala Met Val Ala Arg Ser Ser Asp Leu Pro
845 850 855

Tyr Leu Ile Val Gly Val Val Leu Gly Ser Ile Val Leu Ile Ile
860 865 870

Val Thr Phe Ile Pro Phe Cys Leu Trp Arg Ala Trp Ser Lys Gln
875 880 885

Lys His Thr Thr Asp Leu Gly Phe Pro Arg Ser Ala Leu Pro Pro
890 895 900

Ser Cys Pro Tyr Thr Met Val Pro Leu Gly Gly Leu Pro Gly His
905 910 915

Gln Ala Ser Gly Gln Pro Tyr Leu Ser Gly Ile Ser Gly Arg Ala
920 925 930

Cys Ala Asn Gly Ile His Met Asn Arg Gly Cys Pro Ser Ala Ala
935 940 945

Val Gly Tyr Pro Gly Met Lys Pro Gln Gln His Cys Pro Gly Glu
950 955 960

Leu Gln Gln Gln Ser Asp Thr Ser Ser Leu Leu Arg Gln Thr His
965 970 975

Leu Gly Asn Gly Tyr Asp Pro Gln Ser His Gln Ile Thr Arg Gly
980 985 990

Pro Lys Ser Ser Pro Asp Glu Gly Ser Phe Leu Tyr Thr Leu Pro
995 1000 1005

Asp Asp Ser Thr His Gln Leu Leu Gln Pro His His Asp Cys Cys
1010 1015 1020

Gln Arg Gln Glu Gln Pro Ala Ala Val Gly Gln Ser Gly Val Arg
1025 1030 1035

Arg Ala Pro Asp Ser Pro Val Leu Glu Ala Val Trp Asp Pro Pro
1040 1045 1050

Phe His Ser Gly Pro Pro Cys Cys Leu Gly Leu Val Pro Val Glu
1055 1060 1065

Glu Val Asp Ser Pro Asp Ser Cys Gln Val Ser Gly Gly Asp Trp
1070 1075 1080

Cys Pro Gln His Pro Val Gly Ala Tyr Val Gly Gln Glu Pro Gly
1085 1090 1095

Met Gln Leu Ser Pro Gly Pro Leu Val Arg Val Ser Phe Glu Thr
1100 1105 1110

Pro Pro Leu Thr Ile
1115

<210> 59
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 59
gggaaacaca gcagtcatcg cctgc 25

<210> 60
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 60
gcacacgttag cctgtcgctg gagc 24

<210> 61
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe.

<400> 61
caccccaaag cccaggatccg gtacagcgta aaacaagagt gg 42

<210> 62
<211> 1661
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 678
<223> unknown base

<400> 62
cgggaggctg ggtcgcatg atccggaccc cattgtcgcc ctctgccc 50
ccctgctcc tcccaggctc ccgcggccga cccccgcgca acatgcagcc 100
cacgggccgc gagggttccc gcgcgctca ag ccggcggtat ctgcggcg 150
tgctgctcct gctactgctg ctgctgctgc ggcagccgt aacccgcg 200
gagaccacgc cgggcgcccc cagagccctc tccacgctgg gtc 250
ccttttacc accgcgggtg tccccagcgc cctcaactacc ccaggcctca 300
ctacgccagg caccccaaa accctggacc ttgggggtcg cgccgaggcc 350
ctgatgcgga gttccact cgtggacggc cacaatgacc tgccccaggt 400
cctgagacag cgttacaaga atgtgcttca ggatgttaac ctgcgaaatt 450
tcagccatgg tcagaccaggc ctggacaggc ttagagacgg cctcggtt 500
gcccaaggctt ggtcgccctc cgtctcatgc cagtcaggc accagactgc 550
cgtgcgcctc gccctggagc agattgaccc tattcaccgc atgtgtgc 600
cctactctga actcgagctt gtgacccctca ctgaaggctt gaacagctt 650
caaaagctgg cctgcctcat tggcgtgnag ggtggtcact cactggacag 700
cagcctctct gtgctgcgca gttctatgt gctgggggtg cgctacctga 750
cacttacctt cacctgcagt acaccatggg cagagagttc caccaagttc 800
agacaccaca tgtacaccaa cgtcagcgga ttgacaagct ttgggtgagaa 850

agtagtagag gagttgaacc gcctggcat gatgatagat ttgtcctatg 900
catcgacac cttgataaga agggtcctgg aagtgtctca ggctcctgtg 950
atcttctccc actcagctgc cagagctgtg tgtgacaatt tgttgaatgt 1000
tcccgatgat atcctgcagc ttctgaagaa cggtggcatc gtgatggta 1050
caactgtccat ggggtgctg cagtgcacc tgcttgctaa cgtgtccact 1100
gtggcagatc actttgacca catcaggca gtcattggat ctgagttcat 1150
cgggatttgtt gaaaaattatg acgggactgg ccgggtccct caggggctgg 1200
aggatgtgtc cacataccca gtcctgataag aggagttgct gagtcgtasc 1250
tggagcgagg aagagcttca aggtgtcctt cgtggaaacc tgctgcgggt 1300
cttcagacaa gtggaaaagg tgagagagga gagcaggcg cagagcccc 1350
tggaggctga gttccatat gggcaactga gcacatcctg ccactccac 1400
ctcgtgcctc agaatggaca ccaggctact catctggagg tgaccaagca 1450
gccaaccaat cgggtccct ggaggtcctc aaatgcctcc ccataccctt 1500
ttcaggcct tggctgtc gccaccatcc caacccac ccagtggctc 1550
tgctgacaca gtcggcccc gcagaggtca ctgtggcaaa gcctcacaaa 1600
gccccctctc ctagttcatt cacaaggata tgctgagaat aaacatgtta 1650
cacatggaaa a 1661

<210> 63
<211> 487
<212> PRT
<213> Homo sapiens

<220>
<221> unsure
<222> 196, 386
<223> unknown amino acid

<400> 63
Met Gln Pro Thr Gly Arg Glu Gly Ser Arg Ala Leu Ser Arg Arg
1 5 10 15
Tyr Leu Arg Arg Leu Leu Leu Leu Leu Leu Leu Leu Leu Arg
20 25 30
Gln Pro Val Thr Arg Ala Glu Thr Thr Pro Gly Ala Pro Arg Ala
35 40 45
Leu Ser Thr Leu Gly Ser Pro Ser Leu Phe Thr Thr Pro Gly Val
50 55 60

Pro Ser Ala Leu Thr Thr Pro Gly Leu Thr Thr Pro Gly Thr Pro
65 70 75

Lys Thr Leu Asp Leu Arg Gly Arg Ala Gln Ala Leu Met Arg Ser
80 85 90

Phe Pro Leu Val Asp Gly His Asn Asp Leu Pro Gln Val Leu Arg
95 100 105

Gln Arg Tyr Lys Asn Val Leu Gln Asp Val Asn Leu Arg Asn Phe
110 115 120

Ser His Gly Gln Thr Ser Leu Asp Arg Leu Arg Asp Gly Leu Val
125 130 135

Gly Ala Gln Phe Trp Ser Ala Ser Val Ser Cys Gln Ser Gln Asp
140 145 150

Gln Thr Ala Val Arg Leu Ala Leu Glu Gln Ile Asp Leu Ile His
155 160 165

Arg Met Cys Ala Ser Tyr Ser Glu Leu Glu Leu Val Thr Ser Ala
170 175 180

Glu Gly Leu Asn Ser Ser Gln Lys Leu Ala Cys Leu Ile Gly Val
185 190 195

Xaa Gly Gly His Ser Leu Asp Ser Ser Leu Ser Val Leu Arg Ser
200 205 210

Phe Tyr Val Leu Gly Val Arg Tyr Leu Thr Leu Thr Phe Thr Cys
215 220 225

Ser Thr Pro Trp Ala Glu Ser Ser Thr Lys Phe Arg His His Met
230 235 240

Tyr Thr Asn Val Ser Gly Leu Thr Ser Phe Gly Glu Lys Val Val
245 250 255

Glu Glu Leu Asn Arg Leu Gly Met Met Ile Asp Leu Ser Tyr Ala
260 265 270

Ser Asp Thr Leu Ile Arg Arg Val Leu Glu Val Ser Gln Ala Pro
275 280 285

Val Ile Phe Ser His Ser Ala Ala Arg Ala Val Cys Asp Asn Leu
290 295 300

Leu Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys Asn Gly Gly
305 310 315

Ile Val Met Val Thr Leu Ser Met Gly Val Leu Gln Cys Asn Leu
320 325 330

Leu Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His Ile Arg
335 340 345

Ala Val Ile Gly Ser Glu Phe Ile Gly Ile Gly Gly Asn Tyr Asp
350 355 360
Gly Thr Gly Arg Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr
365 370 375
Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Xaa Trp Ser Glu Glu
380 385 390
Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg
395 400 405
Gln Val Glu Lys Val Arg Glu Glu Ser Arg Ala Gln Ser Pro Val
410 415 420
Glu Ala Glu Phe Pro Tyr Gly Gln Leu Ser Thr Ser Cys His Ser
425 430 435
His Leu Val Pro Gln Asn Gly His Gln Ala Thr His Leu Glu Val
440 445 450
Thr Lys Gln Pro Thr Asn Arg Val Pro Trp Arg Ser Ser Asn Ala
455 460 465
Ser Pro Tyr Leu Val Pro Gly Leu Val Ala Ala Ala Thr Ile Pro
470 475 480
Thr Phe Thr Gln Trp Leu Cys
485

<210> 64
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 64
ccttcacctg cagtacacca tgggc 25

<210> 65
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 65
gtcacacaca gctctggcag ctgag 25

<210> 66
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 66
ccaagttcag acaccacatg tacaccaacg tcagcgatt gacaagc 47

<210> 67
<211> 1564
<212> DNA
<213> Homo sapiens

<400> 67
tgctaggctc tgtcccacaa tgcacccgag agcaggagct gaaaggctct 50
aacacccaca gatccctcta tgactgcaat gtgaggtgtc cggctttgct 100
ggcccagcaa gcctgataag catgaagctc ttatcttgg tggctgttgt 150
cgggtgtttg ctgggtcccc cagctgaagc caacaagagt tctgaagata 200
tccggtgcaa atgcacatctgt ccacacccata gaaacatcag tggcacatt 250
tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtggtgg 300
gcccatgcca gtgcctggcc atgacgtgg 99 ggcctactgc ctgctgtgcg 350
agtgcaggta cgaggagcgc agcaccacca ccatcaaggt catcattgtc 400
atctacctgt ccgtgggg tggctgttg ctctacatgg ctttcctgat 450
gctgggtggac cctctgatcc gaaagccgga tgcatacact gagcaactgc 500
acaatgagga ggagaatgag gatgctcgct ctatggcagc agctgctgca 550
tccctcgaaaa gaccccgagc aaacacagtc ctggagcgtg tggaaagggtgc 600
ccagcagcgg tggaaagctgc aggtgcagga gcagcggaaag acagtcttcg 650
atcggcacaa gatgctcagc tagatggct ggtgtgggtt ggtcaaggcc 700
ccaacacccat ggctgccagc ttccaggctg gacaaagcag ggggctactt 750
ctcccttccc tcgggttccag tcttccctt aaaaggctgt ggcattttc 800
ctccttctcc ctaacttttag aaatgttgta cttggctatt ttgatttaggg 850
aagaggatg tggctctga tctctgttgc cttctgggtt ctttgggtt 900
gaaggggagg ggaaggcagg ccagaaggaa atggagacat tcgaggcggc 950
ctcaggagtg gatgcgatct gtctctcctg gctccactct tgccgccttc 1000
cagctctgag tcttggaaat gtgttaccc ttggaaagata aagctgggtc 1050
ttcaggaact cagtgtctgg gaggaaagca tggccagca ttcagcatgt 1100
gttcctttct gcagtgggtc ttatcaccac ctccctccca gccccggcgc 1150

ctcagccccca gccccagctc cagccctgag gacagctctg atgggagagc 1200
tggggcccccct gagcccactg ggtcttcagg gtgcactgga agctggtgtt 1250
cgctgtcccc tgtgcacttc tcgcactggg gcatggagtg cccatgcata 1300
ctctgctgcc ggtcccctca cctgcacttg aggggtctgg gcagtcctc 1350
ctctccccag tgtccacagt cactgagcca gacggtcggt tggaacatga 1400
gactcgaggc tgagcgtgga tctgaacacc acagccctg tacttgggtt 1450
gcctcttgtc cctgaacttc gttgtaccag tgcattggaga gaaaatttg 1500
tcctcttgtc tttagagttgt gtgtaaatca aggaagccat cattaaattg 1550
ttttatttct ctca 1564

<210> 68
<211> 183
<212> PRT
<213> Homo sapiens

<400> 68
Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val
1 5 10 15

Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys
20 25 30

Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn
35 40 45

Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu
50 55 60

Pro Met Pro Val Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu
65 70 75

Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr Ile Lys Val
80 85 90

Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu Leu Leu Tyr
95 100 105

Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys Pro Asp
110 115 120

Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Asn Glu Asp Ala
125 130 135

Arg Ser Met Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala
140 145 150

Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys
155 160 165

Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe Asp Arg His Lys
170 175 180

Met Leu Ser

<210> 69
<211> 3170
<212> DNA
<213> Homo sapiens

<400> 69
agcgggtctc gcttgggttc cgctaatttc tgtcctgagg cgtgagactg 50
agtcatagg gtcctggtc cccgaaccag gaagggttga ggaaacacaa 100
tctgcaagcc cccgcgaccc aagtgagggg ccccgtgttgc ggtcctccc 150
tcccttgca ttccccaccc tccgggcttt gcgtttcctt ggggacccccc 200
tcgcccggag atggccgcgt tgatgcggag caaggattcg tcctgctgcc 250
tgctcctact ggccgcgttgc ctgatggtgg agagctcaca gatcggcagt 300
tcgcgggcca aactcaactc catcaagtcc tctctggcgt gggagacgcc 350
tggtcaggcc gccaatcgat ctgcgggcat gtaccaagga ctggcattcg 400
gcggcagtaa gaaggcataa aacctggggc aggccctaccc ttgttagcagt 450
gataaggagt gtgaaggttgg gaggtattgc cacagtcccc accaaggatc 500
atcggcctgc atggtgtgtc ggagaaaaaa gaagcgctgc caccgagatg 550
gcatgtgctg ccccagtagcc cgctgcaata atggcatctg tatcccagtt 600
actgaaagca tcttaacccca tcacatcccc gctctggatg gtactcggca 650
cagagatcga aaccacggtc attactcaaa ccatgacttg ggatggcaga 700
atctaggaag accacacact aagatgtcac atataaaagg gcatgaagga 750
gaccctgcc tacgatcatc agactgcatt gaagggttt gctgtgctcg 800
tcatttctgg accaaaatct gcaaaccagt gctccatcag gggaaagtct 850
gtaccaaaca acgcaagaag gttctcatg ggctggaaat tttccagcgt 900
tgcgactgtg cgaaggccct gtcttgcaaa gtatggaaag atgccaccta 950
ctcctccaaa gccagactcc atgtgtgtca gaaaatttga tcaccattga 1000
ggaacatcat caattgcaga ctgtgaagtt gtgtatttaa tgcattatag 1050
catggtgaa aataaggttc agatgcagaa gaatggctaa aataagaaac 1100

gtgataagaa tatagatgtat cacaagg gagaaagaaa acatgaactg 1150
aatagattag aatgggtgac aaatgcagtgcagccagtgtttcattatg 1200
caacttgtct atgttataa tgtacacatt tgtggaaat gctattat 1250
agagaacaag cacacagtgg aaattactga tgtagtagcat gtgactttcc 1300
aagagtttag gttgtgctgg aggagaggtt tccttcagat tgctgattgc 1350
ttatacaaataat aacctacatg ccagatttctt attcaacgtt agagtttaac 1400
aaaatactcc tagaataact ttttatacaa taggttctaa aaataaaatt 1450
gctaaacaag aaatgaaaac atggaggcatt gttaatttac aacagaaaat 1500
taccttttga tttgttaaac tacttctgct gttcaatcaa gagtcttggt 1550
agataagaaa aaaatcagtc aatatttcca aataattgca aaataatggc 1600
cagttgttta ggaaggcctt taggaagaca aataaataac aaacaaacag 1650
ccacaaatac tttttttca aaatttttagt tttacctgtt attaataaga 1700
actgatacaa gacaaaaaca gttccttcag attctacgga atgacagtat 1750
atctctctt atcctatgttgcatttgc tgaatgcattt atattttcca 1800
aactataccc ataaattgttgcactgataaa tacttacaca gagcagaatt 1850
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gctaacagag agatcattat ttcttaaaga ttggccataa cctatatttt 1950
gatagaatta gattggtaaa tacatgttattt catacatact ctgtggtaat 2000
agagacttaa gctggatctg tactgcactg gagtaagcaa gaaaattggg 2050
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tcagtgtgag gtcctgtgtc cgtaatcc tcaaatttatttattttatag 2250
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tcctgaagta gacagagtag tgaggtttca ttgcctcta taagcttctg 2350
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accacagttt ctaaattctt tggaaaccact ttactactt ttttaaactt 2550

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tcttttactt aaatcccatc tgcatctca aatttaagtt ctcccagtag 2700
agattgagtt tgagcctgta tatctattaa aaatttcaac ttcccacata 2750
tatttactaa gatgattaag acttacattt tctgcacagg tctgcaaaaa 2800
caaaaattat aaactagtcc atccaagaac caaagtttgt ataaacaggt 2850
tgctataagc ttgtgaaatg aaaatggaac atttcaatca aacatttcct 2900
atataacaat tattatattt acaatttggt ttctgcaata tttttcttat 2950
gtccaccctt ttaaaaatta ttatttgaag taatttattt acaggaaatg 3000
ttaatgagat gtatttctt atagagatat ttcttacaga aagctttgta 3050
gcagaatata tttcgagcta ttgactttgt aattnaggaa aaatgtataa 3100
taagataaaa tctattaaat ttttctcctc taaaaactga aaaaaaaaaa 3150
aaaaaaaaaa aaaaaaaaaa 3170

<210> 70
<211> 259
<212> PRT
<213> Homo sapiens

<400> 70
Met Ala Ala Leu Met Arg Ser Lys Asp Ser Ser Cys Cys Leu Leu
1 5 10 15

Leu Leu Ala Ala Val Leu Met Val Glu Ser Ser Gln Ile Gly Ser
20 25 30

Ser Arg Ala Lys Leu Asn Ser Ile Lys Ser Ser Leu Gly Gly Glu
35 40 45

Thr Pro Gly Gln Ala Ala Asn Arg Ser Ala Gly Met Tyr Gln Gly
50 55 60

Leu Ala Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala
65 70 75

Tyr Pro Cys Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys
80 85 90

His Ser Pro His Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg
95 100 105

Lys Lys Lys Arg Cys His Arg Asp Gly Met Cys Cys Pro Ser Thr
110 115 120

Arg Cys Asn Asn Gly Ile Cys Ile Pro Val Thr Glu Ser Ile Leu
125 130 135
Thr Pro His Ile Pro Ala Leu Asp Gly Thr Arg His Arg Asp Arg
140 145 150
Asn His Gly His Tyr Ser Asn His Asp Leu Gly Trp Gln Asn Leu
155 160 165
Gly Arg Pro His Thr Lys Met Ser His Ile Lys Gly His Glu Gly
170 175 180
Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly Phe Cys Cys
185 190 195
Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu His Gln
200 205 210
Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly Leu
215 220 225
Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys
230 235 240
Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val
245 250 255
Cys Gln Lys Ile

<210> 71
<211> 1809
<212> DNA
<213> Homo sapiens

<400> 71
tctcaatctg ctgacacctcgatccgcctg accttgtaat ccacctacct 50
tggcctccca aagtgttggg attacaggcg tgagccaccc cgcccgccca 100
acatcacgtt tttaaaaatt gatttcttca aattcatggc aaatatttcc 150
cttcccttta acttcttatg tcagaatgag gaaggatagc tgcatttatt 200
tagtcagttt tcattgcata gtaatatttt catgtatgtat tttctaagtt 250
atattttagt aattcatatg ttttagatta taggtttaa catacttg 300
aaaatacttg atgtgttta aagccttggg cagaaattct gtattgttga 350
ggatttgttc ttttatcccc cttttaaagt catccgtcct tggctcagga 400
tttggagagc ttgcaccacc aaaaatggca aacatcacca gctcccagat 450
tttggaccag ttgaaagctc cgagtttggg ccagtttacc accaccccaa 500
gtacacagca gaatagtaca agtcacccta caactactac ttcttggac 550

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ctgaaaaga 1809

<210> 72
<211> 363
<212> PRT
<213> Homo sapiens

<400> 72
Met Cys Phe Lys Ala Leu Gly Arg Asn Ser Val Leu Leu Arg Ile
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Cys Ser Phe Ile Pro Leu Leu Lys Ser Ser Val Leu Gly Ser Gly
20 25 30

Phe Gly Glu Leu Ala Pro Pro Lys Met Ala Asn Ile Thr Ser Ser
35 40 45

Gln Ile Leu Asp Gln Leu Lys Ala Pro Ser Leu Gly Gln Phe Thr
50 55 60

Thr Thr Pro Ser Thr Gln Gln Asn Ser Thr Ser His Pro Thr Thr
65 70 75

Thr Thr Ser Trp Asp Leu Lys Pro Pro Thr Ser Gln Ser Ser Val
80 85 90

Leu Ser His Leu Asp Phe Lys Ser Gln Pro Glu Pro Ser Pro Val
95 100 105

Leu Ser Gln Leu Ser Gln Arg Gln Gln His Gln Ser Gln Ala Val
110 115 120

Thr Val Pro Pro Pro Gly Leu Glu Ser Phe Pro Ser Gln Ala Lys
125 130 135

Leu Arg Glu Ser Thr Pro Gly Asp Ser Pro Ser Thr Val Asn Lys
140 145 150

Leu Leu Gln Leu Pro Ser Thr Thr Ile Glu Asn Ile Ser Val Ser
155 160 165

Val His Gln Pro Gln Pro Lys His Ile Lys Leu Ala Lys Arg Arg
170 175 180

Ile Pro Pro Ala Ser Lys Ile Pro Ala Ser Ala Val Glu Met Pro
185 190 195

Gly Ser Ala Asp Val Thr Gly Leu Asn Val Gln Phe Gly Ala Leu
200 205 210

Glu Phe Gly Ser Glu Pro Ser Leu Ser Glu Phe Gly Ser Ala Pro
215 220 225

Ser Ser Glu Asn Ser Asn Gln Ile Pro Ile Ser Leu Tyr Ser Lys
230 235 240

Ser Leu Ser Glu Pro Leu Asn Thr Ser Leu Ser Met Thr Ser Ala
245 250 255

Val Gln Asn Ser Thr Tyr Thr Ser Val Ile Thr Ser Cys Ser
260 265 270

Leu Thr Ser Ser Ser Leu Asn Ser Ala Ser Pro Val Ala Met Ser

275 280 285
Ser Ser Tyr Asp Gln Ser Ser Val His Asn Arg Ile Pro Tyr Gln
290 295 300
Ser Pro Val Ser Ser Ser Glu Ser Ala Pro Gly Thr Ile Met Asn
305 310 315
Gly His Gly Gly Gly Arg Ser Gln Gln Thr Leu Asp Ser Lys Tyr
320 325 330
Ser Ser Lys Leu Leu Leu Ser Trp Leu Val Pro Thr Lys Gln Arg
335 340 345
Lys Arg Ile Ala His Val Met Trp Lys Thr Pro Val Gly Gln Trp
350 355 360
Leu Ile Arg

<210> 73
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 73
aattcatggc aaatatttcc cttccc 26

<210> 74
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 74
tggtaaactg gcccaaactc gg 22

<210> 75
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 75
ttaaagtcat ccgtccttgg ctcaggattt ggagagcttg caccaccaaa 50

<210> 76
<211> 1989
<212> DNA
<213> Homo sapiens

<400> 76
cccgagtgaa acaaaggctg gggctggcgc gggccatgg cgctgccatc 50
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tgcaactcagc ggtggaggag acggacgcgg ggctgtacac ctgcaacctg 150
caccatcaact actgccaccc tctacgagac ctggccgtcc gcctggaggt 200
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ccactctcag cacccacat ttgcacatgc tggtaggaccc gccaaccatca 1950
caataaaagtc cccatctgat ttttaaaaaa aaaaaaaaa 1989

<210> 77

<211> 341

<212> PRT

<213> Homo sapiens

<400> 77

Met Ala Leu Pro Ser Arg Ile Leu Leu Trp Lys Leu Val Leu Leu
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Gln Ser Ser Ala Val Leu Leu His Ser Ala Val Glu Glu Thr Asp
20 25 30

Ala Gly Leu Tyr Thr Cys Asn Leu His His His Tyr Cys His Leu
35 40 45

Tyr Glu Ser Leu Ala Val Arg Leu Glu Val Thr Asp Gly Pro Pro
50 55 60

Ala Thr Pro Ala Tyr Trp Asp Gly Glu Lys Glu Val Leu Ala Val
65 70 75

Ala Arg Gly Ala Pro Ala Leu Leu Thr Cys Val Asn Arg Gly His
80 85 90

Val Trp Thr Asp Arg His Val Glu Glu Ala Gln Gln Val Val His
95 100 105

Trp Asp Arg Gln Pro Pro Gly Val Pro His Asp Arg Ala Asp Arg
110 115 120

Leu Leu Asp Leu Tyr Ala Ser Gly Glu Arg Arg Ala Tyr Gly Pro
125 130 135

Leu Phe Leu Arg Asp Arg Val Ala Val Gly Ala Asp Ala Phe Glu
140 145 150

Arg Gly Asp Phe Ser Leu Arg Ile Glu Pro Leu Glu Val Ala Asp
155 160 165

Glu Gly Thr Tyr Ser Cys His Leu His His Tyr Cys Gly Leu
170 175 180

His Glu Arg Arg Val Phe His Leu Thr Val Ala Glu Pro His Ala
185 190 195

Glu Pro Pro Pro Arg Gly Ser Pro Gly Asn Gly Ser Ser His Ser
200 205 210

Gly Ala Pro Gly Pro Asp Pro Thr Leu Ala Arg Gly His Asn Val
215 220 225

Ile Asn Val Ile Val Pro Glu Ser Arg Ala His Phe Phe Gln Gln
230 235 240

Leu Gly Tyr Val Leu Ala Thr Leu Leu Leu Phe Ile Leu Leu Leu
245 250 255

Val Thr Val Leu Leu Ala Ala Arg Arg Arg Arg Gly Gly Tyr Glu
260 265 270

Tyr Ser Asp Gln Lys Ser Gly Lys Ser Lys Gly Lys Asp Val Asn
275 280 285

Leu Ala Glu Phe Ala Val Ala Ala Gly Asp Gln Met Leu Tyr Arg
290 295 300

Ser Glu Asp Ile Gln Leu Asp Tyr Lys Asn Asn Ile Leu Lys Glu
305 310 315

Arg Ala Glu Leu Ala His Ser Pro Leu Pro Ala Lys Tyr Ile Asp
320 325 330

Leu Asp Lys Gly Phe Arg Lys Glu Asn Cys Lys
335 340

<210> 78
<211> 2243
<212> DNA
<213> Homo sapiens

<400> 78
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cagtctccga gctgaccagg aggcactgct tgagaagctg ctggaccgcc 150
cgccccctgg cctgcagagg cccgaggacc gtttctgtgg cacatacatc 200

atcttcttca gcctggcat tggcagtcta ctgccatgga acttctttat 250
cactgccaag gagtaactgga tttcaaaact ccgcaactcc tccagcccag 300
ccaccgggaa ggaccctgag ggctcagaca tcctgaacta ctttgagagc 350
taccttgccg ttgcctccac cgtgcctcc atgctgtgcc tggtgccaa 400
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tgacggtcat cctggccatc ttcatggtga taactgcact ggtgaaggtg 500
gacacttcct cctggacccg tggtttttt gcggtcacca ttgtctgcat 550
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gccattggtt caagggcgta ataaatactt gcgtattcaa aaa 2243

<210> 79

<211> 475

<212> PRT

<213> Homo sapiens

<400> 79

Met Ala Val Val Ser Glu Asp Asp Phe Gln His Ser Ser Asn Ser
1 5 10 15

Thr Tyr Gly Thr Thr Ser Ser Ser Leu Arg Ala Asp Gln Glu Ala
20 25 30

Leu Leu Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg
35 40 45

Pro Glu Asp Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu
50 55 60

Gly Ile Gly Ser Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys
65 70 75

Glu Tyr Trp Met Phe Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr
80 85 90

Gly Glu Asp Pro Glu Gly Ser Asp Ile Leu Asn Tyr Phe Glu Ser
95 100 105

Tyr Leu Ala Val Ala Ser Thr Val Pro Ser Met Leu Cys Leu Val
110 115 120

Ala Asn Phe Leu Leu Val Asn Arg Val Ala Val His Ile Arg Val
125 130 135

Leu Ala Ser Leu Thr Val Ile Leu Ala Ile Phe Met Val Ile Thr
140 145 150

Ala Leu Val Lys Val Asp Thr Ser Ser Trp Thr Arg Gly Phe Phe
155 160 165

Ala Val Thr Ile Val Cys Met Val Ile Leu Ser Gly Ala Ser Thr
170 175 180

Val Phe Ser Ser Ser Ile Tyr Gly Met Thr Gly Ser Phe Pro Met
185 190 195

Arg Asn Ser Gln Ala Leu Ile Ser Gly Gly Ala Met Gly Gly Thr
200 205 210

Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala Ala Ser Ser Asp
215 220 225

Val Arg Asn Ser Ala Leu Ala Phe Phe Leu Thr Ala Thr Ile Phe
230 235 240

Leu Val Leu Cys Met Gly Leu Tyr Leu Leu Leu Ser Arg Leu Glu
245 250 255

Tyr Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala Ala His Val Phe
260 265 270

Ser Gly Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser Ala Pro Ser
275 280 285

Val Ala Ser Arg Phe Ile Asp Ser His Thr Pro Pro Leu Arg Pro
290 295 300

Ile Leu Lys Lys Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr Val
305 310 315

Phe Phe Ile Thr Ser Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile
320 325 330

Glu Ser Leu Asn Lys Gly Ser Gly Ser Leu Trp Thr Thr Lys Phe
335 340 345

Phe Ile Pro Leu Thr Thr Phe Leu Leu Tyr Asn Phe Ala Asp Leu
350 355 360

Cys Gly Arg Gln Leu Thr Ala Trp Ile Gln Val Pro Gly Pro Asn
365 370 375

Ser Lys Ala Leu Pro Gly Phe Val Leu Leu Arg Thr Cys Leu Ile
380 385 390

Pro Leu Phe Val Leu Cys Asn Tyr Gln Pro Arg Val His Leu Lys
395 400 405

Thr Val Val Phe Gln Ser Asp Val Tyr Pro Ala Leu Leu Ser Ser
410 415 420

Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu Ala Leu Leu
425 430 435

Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala Thr Gly
440 445 450

Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly Ser
455 460 465

Ala Cys Ser Thr Leu Leu Val His Leu Ile
470 475

<210> 80

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 80

tttgccgtc accattgtct gc 22

<210> 81

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 81

cgttaggtgac acagaagccc agg 23

<210> 82

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 82

tacggcatga ccggctcctt tcctatgagg aactcccagg cactgatat 49

<210> 83

<211> 1844

<212> DNA

<213> Homo sapiens

<400> 83

gacagtggag ggcagtggag aggaccgcgc tgtccctgctg tcaccaagag 50

ctggagacac catctccac cgagagtcat ggccccattg gccctgcacc 100

tcctcgatc cgtccccatc ctccctcagcc tggtgccctc ccaggactgg 150

aaggctgaac gcagccaaga ccccttcgag aaatgcattgc aggatcctga 200
ctatgagcag ctgtcaagg tggtgacctg ggggctcaat cggaccctga 250
agccccagag ggtgattgtg gttggcgctg gtgtggccgg gctggtgccc 300
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aaaacacgac ccacacgagg acctcgatt aaagtattt cgaaaaaaa 1800
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1844

<210> 84
<211> 567
<212> PRT
<213> Homo sapiens

<400> 84
Met Ala Pro Leu Ala Leu His Leu Leu Val Leu Val Pro Ile Leu
1 5 10 15
Leu Ser Leu Val Ala Ser Gln Asp Trp Lys Ala Glu Arg Ser Gln
20 25 30
Asp Pro Phe Glu Lys Cys Met Gln Asp Pro Asp Tyr Glu Gln Leu
35 40 45
Leu Lys Val Val Thr Trp Gly Leu Asn Arg Thr Leu Lys Pro Gln
50 55 60
Arg Val Ile Val Val Gly Ala Gly Val Ala Gly Leu Val Ala Ala
65 70 75
Lys Val Leu Ser Asp Ala Gly His Lys Val Thr Ile Leu Glu Ala
80 85 90
Asp Asn Arg Ile Gly Gly Arg Ile Phe Thr Tyr Arg Asp Gln Asn
95 100 105
Thr Gly Trp Ile Gly Glu Leu Gly Ala Met Arg Met Pro Ser Ser
110 115 120
His Arg Ile Leu His Lys Leu Cys Gln Gly Leu Gly Leu Asn Leu
125 130 135
Thr Lys Phe Thr Gln Tyr Asp Lys Asn Thr Trp Thr Glu Val His
140 145 150
Glu Val Lys Leu Arg Asn Tyr Val Val Glu Lys Val Pro Glu Lys
155 160 165
Leu Gly Tyr Ala Leu Arg Pro Gln Glu Lys Gly His Ser Pro Glu
170 175 180
Asp Ile Tyr Gln Met Ala Leu Asn Gln Ala Leu Lys Asp Leu Lys
185 190 195

Ala Leu Gly Cys Arg Lys Ala Met Lys Lys Phe Glu Arg His Thr
200 205 210

Leu Leu Glu Tyr Leu Leu Gly Glu Gly Asn Leu Ser Arg Pro Ala
215 220 225

Val Gln Leu Leu Gly Asp Val Met Ser Glu Asp Gly Phe Phe Tyr
230 235 240

Leu Ser Phe Ala Glu Ala Leu Arg Ala His Ser Cys Leu Ser Asp
245 250 255

Arg Leu Gln Tyr Ser Arg Ile Val Gly Gly Trp Asp Leu Leu Pro
260 265 270

Arg Ala Leu Leu Ser Ser Leu Ser Gly Leu Val Leu Leu Asn Ala
275 280 285

Pro Val Val Ala Met Thr Gln Gly Pro His Asp Val His Val Gln
290 295 300

Ile Glu Thr Ser Pro Pro Ala Arg Asn Leu Lys Val Leu Lys Ala
305 310 315

Asp Val Val Leu Leu Thr Ala Ser Gly Pro Ala Val Lys Arg Ile
320 325 330

Thr Phe Ser Pro Pro Leu Pro Arg His Met Gln Glu Ala Leu Arg
335 340 345

Arg Leu His Tyr Val Pro Ala Thr Lys Val Phe Leu Ser Phe Arg
350 355 360

Arg Pro Phe Trp Arg Glu Glu His Ile Glu Gly Gly His Ser Asn
365 370 375

Thr Asp Arg Pro Ser Arg Met Ile Phe Tyr Pro Pro Pro Arg Glu
380 385 390

Gly Ala Leu Leu Leu Ala Ser Tyr Thr Trp Ser Asp Ala Ala Ala
395 400 405

Ala Phe Ala Gly Leu Ser Arg Glu Glu Ala Leu Arg Leu Ala Leu
410 415 420

Asp Asp Val Ala Ala Leu His Gly Pro Val Val Arg Gln Leu Trp
425 430 435

Asp Gly Thr Gly Val Val Lys Arg Trp Ala Glu Asp Gln His Ser
440 445 450

Gln Gly Gly Phe Val Val Gln Pro Pro Ala Leu Trp Gln Thr Glu
455 460 465

Lys Asp Asp Trp Thr Val Pro Tyr Gly Arg Ile Tyr Phe Ala Gly
470 475 480

Glu His Thr Ala Tyr Pro His Gly Trp Val Glu Thr Ala Val Lys
485 490 495
Ser Ala Leu Arg Ala Ala Ile Lys Ile Asn Ser Arg Lys Gly Pro
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Ala Ser Asp Thr Ala Ser Pro Glu Gly His Ala Ser Asp Met Glu
515 520 525
Gly Gln Gly His Val His Gly Val Ala Ser Ser Pro Ser His Asp
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Ser Leu Gln Asn Thr Thr His Thr Arg Thr Ser His
560 565

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<213> Homo sapiens

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<210> 86

<211> 739

<212> PRT

<213> Homo sapiens

<400> 86

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Gly Ser Pro His Ser Leu Glu Ala Leu Arg Asp Ala Ala Pro Ser

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Gln	Gly	Leu	Asn	Phe	Leu	Leu	Leu	Phe	Thr	Lys	Met	Leu	Phe	Ile
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Phe	Asn	Phe	Leu	Phe	Ser	Pro	Leu	Pro	Thr	Pro	Ala	Leu	Ile	Cys
		65							70					75
Ile	Leu	Thr	Phe	Gly	Ala	Ala	Ile	Phe	Leu	Trp	Leu	Ile	Thr	Arg
		80							85					90
Pro	Gln	Pro	Val	Leu	Pro	Leu	Leu	Asp	Leu	Asn	Asn	Gln	Ser	Val
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Gly	Ile	Glu	Gly	Gly	Ala	Arg	Lys	Gly	Val	Ser	Gln	Lys	Asn	Asn
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Asp	Leu	Thr	Ser	Cys	Cys	Phe	Ser	Asp	Ala	Lys	Thr	Met	Tyr	Glu
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Val	Phe	Gln	Arg	Gly	Leu	Ala	Val	Ser	Asp	Asn	Gly	Pro	Cys	Leu
		140							145					150
Gly	Tyr	Arg	Lys	Pro	Asn	Gln	Pro	Tyr	Arg	Trp	Leu	Ser	Tyr	Lys
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Gln	Val	Ser	Asp	Arg	Ala	Glu	Tyr	Leu	Gly	Ser	Cys	Leu	Leu	His
		170							175					180
Lys	Gly	Tyr	Lys	Ser	Ser	Pro	Asp	Gln	Phe	Val	Gly	Ile	Phe	Ala
		185							190					195
Gln	Asn	Arg	Pro	Glu	Trp	Ile	Ile	Ser	Glu	Leu	Ala	Cys	Tyr	Thr
		200							205					210
Tyr	Ser	Met	Val	Ala	Val	Pro	Leu	Tyr	Asp	Thr	Leu	Gly	Pro	Glu
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Ala	Ile	Val	His	Ile	Val	Asn	Lys	Ala	Asp	Ile	Ala	Met	Val	Ile
		230							235					240
Cys	Asp	Thr	Pro	Gln	Lys	Ala	Leu	Val	Leu	Ile	Gly	Asn	Val	Glu
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Lys	Gly	Phe	Thr	Pro	Ser	Leu	Lys	Val	Ile	Ile	Leu	Met	Asp	Pro
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Phe	Asp	Asp	Asp	Leu	Lys	Gln	Arg	Gly	Glu	Lys	Ser	Gly	Ile	Glu
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Ile	Leu	Ser	Leu	Tyr	Asp	Ala	Glu	Asn	Leu	Gly	Lys	Glu	His	Phe
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Arg	Lys	Pro	Val	Pro	Pro	Ser	Pro	Glu	Asp	Leu	Ser	Val	Ile	Cys
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Phe	Thr	Ser	Gly	Thr	Thr	Gly	Asp	Pro	Lys	Gly	Ala	Met	Ile	Thr

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His Gln Asn Ile Val Ser Asn Ala Ala Ala Phe Leu Lys Cys Val
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Glu His Ala Tyr Glu Pro Thr Pro Asp Asp Val Ala Ile Ser Tyr
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Leu Pro Leu Ala His Met Phe Glu Arg Ile Val Gln Ala Val Val
365 370 375
Tyr Ser Cys Gly Ala Arg Val Gly Phe Phe Gln Gly Asp Ile Arg
380 385 390
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395 400 405
Ala Val Pro Arg Leu Leu Asn Arg Ile Tyr Asp Lys Val Gln Asn
410 415 420
Glu Ala Lys Thr Pro Leu Lys Lys Phe Leu Leu Lys Leu Ala Val
425 430 435
Ser Ser Lys Phe Lys Glu Leu Gln Lys Gly Ile Ile Arg His Asp
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Ser Phe Trp Asp Lys Leu Ile Phe Ala Lys Ile Gln Asp Ser Leu
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Gly Gly Arg Val Arg Val Ile Val Thr Gly Ala Ala Pro Met Ser
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Thr Ser Val Met Thr Phe Phe Arg Ala Ala Met Gly Cys Gln Val
485 490 495
Tyr Glu Ala Tyr Gly Gln Thr Glu Cys Thr Gly Gly Cys Thr Phe
500 505 510
Thr Leu Pro Gly Asp Trp Thr Ser Gly His Val Gly Val Pro Leu
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Ala Cys Asn Tyr Val Lys Leu Glu Asp Val Ala Asp Met Asn Tyr
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Phe Thr Val Asn Asn Glu Gly Glu Val Cys Ile Lys Gly Thr Asn
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Val Phe Lys Gly Tyr Leu Lys Asp Pro Glu Lys Thr Gln Glu Ala
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Leu Asp Ser Asp Gly Trp Leu His Thr Gly Asp Ile Gly Arg Trp
575 580 585
Leu Pro Asn Gly Thr Leu Lys Ile Ile Asp Arg Lys Lys Asn Ile
590 595 600
Phe Lys Leu Ala Gln Gly Glu Tyr Ile Ala Pro Glu Lys Ile Glu

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Gly Glu Ser Leu Arg Ser Ser Leu Val Gly Val Val Val Pro Asp			
	635	640	645
Thr Asp Val Leu Pro Ser Phe Ala Ala Lys Leu Gly Val Lys Gly			
	650	655	660
Ser Phe Glu Glu Leu Cys Gln Asn Gln Val Val Arg Glu Ala Ile			
	665	670	675
Leu Glu Asp Leu Gln Lys Ile Gly Lys Glu Ser Gly Leu Lys Thr			
	680	685	690
Phe Glu Gln Val Lys Ala Ile Phe Leu His Pro Glu Pro Phe Ser			
	695	700	705
Ile Glu Asn Gly Leu Leu Thr Pro Thr Leu Lys Ala Lys Arg Gly			
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Glu Leu Ser Lys Tyr Phe Arg Thr Gln Ile Asp Ser Leu Tyr Glu			
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His Ile Gln Asp			

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<212> PRT
<213> Homo sapiens

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35 40 45
Phe Leu Leu Val Thr Val Ile Val Asn Ile Lys Leu Ile Leu Asp
50 55 60
Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu
65 70 75
Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg
80 85 90
Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser
95 100 105

Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val Leu
110 115 120

Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val
125 130 135

Leu Asn Gln Ala Thr Gly His Val Met Ala Lys Arg Val Phe Asp
140 145 150

Thr Tyr Ser Pro His Glu Asp Glu Ala Met Val Leu Phe Leu Asn
155 160 165

Met Val Ala Pro Gly Arg Val Leu Ile Cys Thr Val Lys Asp Glu
170 175 180

Gly Ser Phe His Leu Lys Asp Thr Ala Lys Ala Leu Leu Arg Ser
185 190 195

Leu Gly Ser Gln Ala Gly Pro Ala Leu Gly Trp Arg Asp Thr Trp
200 205 210

Ala Phe Val Gly Arg Lys Gly Gly Pro Val Phe Gly Glu Lys His
215 220 225

Ser Lys Ser Pro Ala Leu Ser Ser Trp Gly Asp Pro Val Leu Leu
230 235 240

Lys Thr Asp Val Pro Leu Ser Ser Ala Glu Glu Ala Glu Cys His
245 250 255

Trp Ala Asp Thr Glu Leu Asn Arg Arg Arg Arg Arg Phe Cys Ser
260 265 270

Lys Val Glu Gly Tyr Gly Ser Val Cys Ser Cys Lys Asp Pro Thr
275 280 285

Pro Ile Glu Phe Ser Pro Asp Pro Leu Pro Asp Asn Lys Val Leu
290 295 300

Asn Val Pro Val Ala Val Ile Ala Gly Asn Arg Pro Asn Tyr Leu
305 310 315

Tyr Arg Met Leu Arg Ser Leu Leu Ser Ala Gln Gly Val Ser Pro
320 325 330

Gln Met Ile Thr Val Phe Ile Asp Gly Tyr Tyr Glu Glu Pro Met
335 340 345

Asp Val Val Ala Leu Phe Gly Leu Arg Gly Ile Gln His Thr Pro
350 355 360

Ile Ser Ile Lys Asn Ala Arg Val Ser Gln His Tyr Lys Ala Ser
365 370 375

Leu Thr Ala Thr Phe Asn Leu Phe Pro Glu Ala Lys Phe Ala Val
380 385 390

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Leu	Ser	Gln	Ser	Ile	His	Leu	Leu	Glu	Glu	Asp	Asp	Ser	Leu	Tyr
				410					415					420
Cys	Ile	Ser	Ala	Trp	Asn	Asp	Gln	Gly	Tyr	Glu	His	Thr	Ala	Glu
				425					430					435
Asp	Pro	Ala	Leu	Leu	Tyr	Arg	Val	Glu	Thr	Met	Pro	Gly	Leu	Gly
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Trp	Val	Leu	Arg	Arg	Ser	Leu	Tyr	Lys	Glu	Glu	Leu	Glu	Pro	Lys
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Trp	Pro	Thr	Pro	Glu	Lys	Leu	Trp	Asp	Trp	Asp	Met	Trp	Met	Arg
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Met	Pro	Glu	Gln	Arg	Arg	Gly	Arg	Glu	Cys	Ile	Ile	Pro	Asp	Val
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Ser	Arg	Ser	Tyr	His	Phe	Gly	Ile	Val	Gly	Leu	Asn	Met	Asn	Gly
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Pro	Gly	Val	Gln	Leu	Arg	Asn	Val	Asp	Ser	Leu	Lys	Lys	Glu	Ala
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Tyr	Glu	Val	Glu	Val	His	Arg	Leu	Leu	Ser	Glu	Ala	Glu	Val	Leu
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Asp	His	Ser	Lys	Asn	Pro	Cys	Glu	Asp	Ser	Phe	Leu	Pro	Asp	Thr
				560					565					570
Glu	Gly	His	Thr	Tyr	Val	Ala	Phe	Ile	Arg	Met	Glu	Lys	Asp	Asp
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Asp	Phe	Thr	Thr	Trp	Thr	Gln	Leu	Ala	Lys	Cys	Leu	His	Ile	Trp
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Asp	Leu	Asp	Val	Arg	Gly	Asn	His	Arg	Gly	Leu	Trp	Arg	Leu	Phe
				605					610					615
Arg	Lys	Lys	Asn	His	Phe	Leu	Val	Val	Gly	Val	Pro	Ala	Ser	Pro
				620					625					630
Tyr	Ser	Val	Lys	Lys	Pro	Pro	Ser	Val	Thr	Pro	Ile	Phe	Leu	Glu
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<212> DNA
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<210> 90
<211> 22
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 90
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<210> 91
<211> 24
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 91
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<210> 92
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<212> DNA
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<220>
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<400> 92
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<210> 93
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<212> DNA
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<210> 95

<211> 307

<212> PRT

<213> Homo sapiens

<400> 95

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20 25 30

Ser Glu Glu Arg Leu Lys Leu Val Thr Val Leu Gly Ala Gly Leu
35 40 45

Leu Cys Gly Thr Ala Leu Ala Val Ile Val Pro Glu Gly Val His
50 55 60

Ala Leu Tyr Glu Asp Ile Leu Glu Gly Lys His His Gln Ala Ser
65 70 75

Glu Thr His Asn Val Ile Ala Ser Asp Lys Ala Ala Glu Lys Ser
80 85 90

Val Val His Glu His Ser His Asp His Thr Gln Leu His
95 100 105

Ala Tyr Ile Gly Val Ser Leu Val Leu Gly Phe Val Phe Met Leu
110 115 120

Leu Val Asp Gln Ile Gly Asn Ser His Val His Ser Thr Asp Asp
125 130 135

Pro Glu Ala Ala Arg Ser Ser Asn Ser Lys Ile Thr Thr Thr Leu
140 145 150

Gly Leu Val Val His Ala Ala Ala Asp Gly Val Ala Leu Gly Ala
155 160 165

Ala Ala Ser Thr Ser Gln Thr Ser Val Gln Leu Ile Val Phe Val
170 175 180

Ala Ile Met Leu His Lys Ala Pro Ala Ala Phe Gly Leu Val Ser
185 190 195

Phe Leu Met His Ala Gly Leu Glu Arg Asn Arg Ile Arg Lys His
200 205 210

Leu Leu Val Phe Ala Leu Ala Ala Pro Val Met Ser Met Val Thr
215 220 225
Tyr Leu Gly Leu Ser Lys Ser Ser Lys Glu Ala Leu Ser Glu Val
230 235 240
Asn Ala Thr Gly Val Ala Met Leu Phe Ser Ala Gly Thr Phe Leu
245 250 255
Tyr Val Ala Thr Val His Val Leu Pro Glu Val Gly Gly Ile Gly
260 265 270
His Ser His Lys Pro Asp Ala Thr Gly Gly Arg Gly Leu Ser Arg
275 280 285
Leu Glu Val Ala Ala Leu Val Leu Gly Cys Leu Ile Pro Leu Ile
290 295 300
Leu Ser Val Gly His Gln His
305

<210> 96
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 96
gttgtgggtg aataaaggag ggcag 25

<210> 97
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 97
cttgctcat gttcatggac aactg 25

<210> 98
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 98
ggatgatttc atctccattt gcctgctgtc tctggctatg ttgggtggat 50

<210> 99
<211> 1429

<212> DNA
<213> Homo sapiens

<400> 99
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ctgattttga gatgatggc ttggaaacg ggcgtcgca gatgaagtgc 150
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ggaatcatac actctgaatt gaactggaat cacatattc acaacaggc 1350

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gaaatgtact aaataaaatg tacatctga 1429

<210> 100

<211> 401

<212> PRT

<213> Homo sapiens

<400> 100

Met Met Gly Leu Gly Asn Gly Arg Arg Ser Met Lys Ser Pro Pro
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Leu Val Leu Ala Ala Leu Val Ala Cys Ile Ile Val Leu Gly Phe
20 25 30

Asn Tyr Trp Ile Ala Ser Ser Arg Ser Val Asp Leu Gln Thr Arg
35 40 45

Ile Met Glu Leu Glu Gly Arg Val Arg Arg Ala Ala Ala Glu Arg
50 55 60

Gly Ala Val Glu Leu Lys Lys Asn Glu Phe Gln Gly Glu Leu Glu
65 70 75

Lys Gln Arg Glu Gln Leu Asp Lys Ile Gln Ser Ser His Asn Phe
80 85 90

Gln Leu Glu Ser Val Asn Lys Leu Tyr Gln Asp Glu Lys Ala Val
95 100 105

Leu Val Asn Asn Ile Thr Thr Gly Glu Arg Leu Ile Arg Val Leu
110 115 120

Gln Asp Gln Leu Lys Thr Leu Gln Arg Asn Tyr Gly Arg Leu Gln
125 130 135

Gln Asp Val Leu Gln Phe Gln Lys Asn Gln Thr Asn Leu Glu Arg
140 145 150

Lys Phe Ser Tyr Asp Leu Ser Gln Cys Ile Asn Gln Met Lys Glu
155 160 165

Val Lys Glu Gln Cys Glu Glu Arg Ile Glu Glu Val Thr Lys Lys
170 175 180

Gly Asn Glu Ala Val Ala Ser Arg Asp Leu Ser Glu Asn Asn Asp
185 190 195

Gln Arg Gln Gln Leu Gln Ala Leu Ser Glu Pro Gln Pro Arg Leu
200 205 210

Gln Ala Ala Gly Leu Pro His Thr Glu Val Pro Gln Gly Lys Gly
215 220 225

Asn Val Leu Gly Asn Ser Lys Ser Gln Thr Pro Ala Pro Ser Ser

230	235	240
Glu Val Val Leu Asp Ser Lys Arg Gln Val Glu Lys Glu Glu Thr		
245	250	255
Asn Glu Ile Gln Val Val Asn Glu Glu Pro Gln Arg Asp Arg Leu		
260	265	270
Pro Gln Glu Pro Gly Arg Glu Gln Val Val Glu Asp Arg Pro Val		
275	280	285
Gly Gly Arg Gly Phe Gly Gly Ala Gly Glu Leu Gly Gln Thr Pro		
290	295	300
Gln Val Gln Ala Ala Leu Ser Val Ser Gln Glu Asn Pro Glu Met		
305	310	315
Glu Gly Pro Glu Arg Asp Gln Leu Val Ile Pro Asp Gly Gln Glu		
320	325	330
Glu Glu Gln Glu Ala Ala Gly Glu Gly Arg Asn Gln Gln Lys Leu		
335	340	345
Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu Asn Glu Ala Glu Ser		
350	355	360
Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn Asp Arg Asn Ile		
365	370	375
Asp Val Phe Asn Val Glu Asp Gln Lys Arg Asp Thr Ile Asn Leu		
380	385	390
Leu Asp Gln Arg Glu Lys Arg Asn His Thr Leu		
395	400	

<210> 101
 <211> 3671
 <212> DNA
 <213> Homo sapiens

<400> 101
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 tgccatgggg gagccaaggg aaacctgggg cctgctggat ggcttcccgaa 200
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agtgtataaa aatgataata t 3671

<210> 102

<211> 1089

<212> PRT

<213> Homo sapiens

<400> 102

Met Gln Lys Ala Ser Val Leu Leu Phe Leu Ala Trp Val Cys Phe
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Leu Phe Tyr Ala Gly Ile Ala Leu Phe Thr Ser Gly Phe Leu Leu
20 25 30

Thr Arg Leu Glu Leu Thr Asn His Ser Ser Cys Gln Glu Pro Pro
35 40 45

Gly Pro Gly Ser Leu Pro Trp Gly Ser Gln Gly Lys Pro Gly Ala
50 55 60

Cys Trp Met Ala Ser Arg Phe Ser Arg Val Val Leu Val Leu Ile
65 70 75

Asp Ala Leu Arg Phe Asp Phe Ala Gln Pro Gln His Ser His Val
80 85 90

Pro Arg Glu Pro Pro Val Ser Leu Pro Phe Leu Gly Lys Leu Ser
95 100 105

Ser Leu Gln Arg Ile Leu Glu Ile Gln Pro His His Ala Arg Leu
110 115 120

Tyr Arg Ser Gln Val Asp Pro Pro Thr Thr Thr Met Gln Arg Leu
125 130 135

Lys Ala Leu Thr Thr Gly Ser Leu Pro Thr Phe Ile Asp Ala Gly
140 145 150

Ser Asn Phe Ala Ser His Ala Ile Val Glu Asp Asn Leu Ile Lys
155 160 165

Gln Leu Thr Ser Ala Gly Arg Arg Val Val Phe Met Gly Asp Asp
170 175 180

Thr Trp Lys Asp Leu Phe Pro Gly Ala Phe Ser Lys Ala Phe Phe
185 190 195

Phe Pro Ser Phe Asn Val Arg Asp Leu Asp Thr Val Asp Asn Gly
200 205 210

Ile Leu Glu His Leu Tyr Pro Thr Met Asp Ser Gly Glu Trp Asp
215 220 225

Val Leu Ile Ala His Phe Leu Gly Val Asp His Cys Gly His Lys
230 235 240

His Gly Pro His His Pro Glu Met Ala Lys Lys Leu Ser Gln Met
245 250 255

Asp Gln Val Ile Gln Gly Leu Val Glu Arg Leu Glu Asn Asp Thr
260 265 270

Leu Leu Val Val Ala Gly Asp His Gly Met Thr Thr Asn Gly Asp
275 280 285

His Gly Gly Asp Ser Glu Leu Glu Val Ser Ala Ala Leu Phe Leu
290 295 300

Tyr Ser Pro Thr Ala Val Phe Pro Ser Thr Pro Pro Glu Glu Pro
305 310 315

Glu Val Ile Pro Gln Val Ser Leu Val Pro Thr Leu Ala Leu Leu
320 325 330

Leu Gly Leu Pro Ile Pro Phe Gly Asn Ile Gly Glu Val Met Ala
335 340 345

Glu Leu Phe Ser Gly Gly Glu Asp Ser Gln Pro His Ser Ser Ala
350 355 360

Leu Ala Gln Ala Ser Ala Leu His Leu Asn Ala Gln Gln Val Ser
365 370 375

Arg Phe Leu His Thr Tyr Ser Ala Ala Thr Gln Asp Leu Gln Ala
380 385 390

Lys Glu Leu His Gln Leu Gln Asn Leu Phe Ser Lys Ala Ser Ala
395 400 405

Asp Tyr Gln Trp Leu Leu Gln Ser Pro Lys Gly Ala Glu Ala Thr
410 415 420

Leu Pro Thr Val Ile Ala Glu Leu Gln Gln Phe Leu Arg Gly Ala
425 430 435

Arg Ala Met Cys Ile Glu Ser Trp Ala Arg Phe Ser Leu Val Arg
440 445 450

Met Ala Gly Gly Thr Ala Leu Leu Ala Ala Ser Cys Phe Ile Cys
455 460 465

Leu Leu Ala Ser Gln Trp Ala Ile Ser Pro Gly Phe Pro Phe Cys
470 475 480

Pro Leu Leu Leu Thr Pro Val Ala Trp Gly Leu Val Gly Ala Ile
485 490 495

Ala Tyr Ala Gly Leu Leu Gly Thr Ile Glu Leu Lys Leu Asp Leu
500 505 510

Val Leu Leu Gly Ala Val Ala Ala Val Ser Ser Phe Leu Pro Phe
515 520 525

Leu Trp Lys Ala Trp Ala Gly Trp Gly Ser Lys Arg Pro Leu Ala
530 535 540

Thr Leu Phe Pro Ile Pro Gly Pro Val Leu Leu Leu Leu Leu Phe
545 550 555

Arg Leu Ala Val Phe Phe Ser Asp Ser Phe Val Val Ala Glu Ala
560 565 570

Arg Ala Thr Pro Phe Leu Leu Gly Ser Phe Ile Leu Leu Leu Val
575 580 585

Val Gln Leu His Trp Glu Gly Gln Leu Leu Pro Pro Lys Leu Leu
590 595 600

Thr Met Pro Arg Leu Gly Thr Ser Ala Thr Thr Asn Pro Pro Arg
605 610 615

His Asn Gly Ala Tyr Ala Leu Arg Leu Gly Ile Gly Leu Leu Leu
620 625 630

Cys Thr Arg Leu Ala Gly Leu Phe His Arg Cys Pro Glu Glu Thr
635 640 645

Pro Val Cys His Ser Ser Pro Trp Leu Ser Pro Leu Ala Ser Met
650 655 660

Val Gly Gly Arg Ala Lys Asn Leu Trp Tyr Gly Ala Cys Val Ala
665 670 675

Ala Leu Val Ala Leu Leu Ala Ala Val Arg Leu Trp Leu Arg Arg
680 685 690

Tyr Gly Asn Leu Lys Ser Pro Glu Pro Pro Met Leu Phe Val Arg
695 700 705

Trp Gly Leu Pro Leu Met Ala Leu Gly Thr Ala Ala Tyr Trp Ala
710 715 720

Leu Ala Ser Gly Ala Asp Glu Ala Pro Pro Arg Leu Arg Val Leu
725 730 735

Val Ser Gly Ala Ser Met Val Leu Pro Arg Ala Val Ala Gly Leu
740 745 750

Ala Ala Ser Gly Leu Ala Leu Leu Trp Lys Pro Val Thr Val
755 760 765

Leu Val Lys Ala Gly Ala Gly Ala Pro Arg Thr Arg Thr Val Leu
770 775 780

Thr Pro Phe Ser Gly Pro Pro Thr Ser Gln Ala Asp Leu Asp Tyr
785 790 795

Val Val Pro Gln Ile Tyr Arg His Met Gln Glu Glu Phe Arg Gly
800 805 810

Arg Leu Glu Arg Thr Lys Ser Gln Gly Pro Leu Thr Val Ala Ala
815 820 825

Tyr Gln Leu Gly Ser Val Tyr Ser Ala Ala Met Val Thr Ala Leu
830 835 840

Thr Leu Leu Ala Phe Pro Leu Leu Leu Leu His Ala Glu Arg Ile
845 850 855

Ser Leu Val Phe Leu Leu Leu Phe Leu Gln Ser Phe Leu Leu Leu
860 865 870

His Leu Leu Ala Ala Gly Ile Pro Val Thr Thr Pro Gly Pro Phe
875 880 885

Thr Val Pro Trp Gln Ala Val Ser Ala Trp Ala Leu Met Ala Thr
890 895 900

Gln Thr Phe Tyr Ser Thr Gly His Gln Pro Val Phe Pro Ala Ile
905 910 915

His Trp His Ala Ala Phe Val Gly Phe Pro Glu Gly His Gly Ser
920 925 930

Cys Thr Trp Leu Pro Ala Leu Leu Val Gly Ala Asn Thr Phe Ala
935 940 945

Ser His Leu Leu Phe Ala Val Gly Cys Pro Leu Leu Leu Leu Trp
950 955 960

Pro Phe Leu Cys Glu Ser Gln Gly Leu Arg Lys Arg Gln Gln Pro
965 970 975

Pro Gly Asn Glu Ala Asp Ala Arg Val Arg Pro Glu Glu Glu Glu
980 985 990

Glu Pro Leu Met Glu Met Arg Leu Arg Asp Ala Pro Gln His Phe
995 1000 1005

Tyr Ala Ala Leu Leu Gln Leu Gly Leu Lys Tyr Leu Phe Ile Leu
1010 1015 1020

Gly Ile Gln Ile Leu Ala Cys Ala Leu Ala Ala Ser Ile Leu Arg
1025 1030 1035

Arg His Leu Met Val Trp Lys Val Phe Ala Pro Lys Phe Ile Phe
1040 1045 1050

Glu Ala Val Gly Phe Ile Val Ser Ser Val Gly Leu Leu Leu Gly
1055 1060 1065

Ile Ala Leu Val Met Arg Val Asp Gly Ala Val Ser Ser Trp Phe
1070 1075 1080

Arg Gln Leu Phe Leu Ala Gln Gln Arg
1085

<210> 103

<211> 1743

<212> DNA

<213> Homo sapiens

<400> 103

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gcagttccct gtgtctctgg tggttgcct aaacctgcaa acatcacctt 100

cttatccatc aacatgaaga atgtcctaca atggactcca ccagagggtc 150

ttcaaggagt taaagttact tacactgtgc agtatttcat cacaatttg 200

cccaccagag gtggcactga ctacagatga gaagtccatt tctgttgtcc 250

tgacagctcc agagaagtgg aagagaaatc cagaagacct tcctgtttcc 300

atgcaacaaa tatactccaa tctgaagtat aacgtgtctg tggtaatac 350

taaatcaaac agaacgtggt cccagtgtgt gaccaaccac acgctgggtc 400

tcacctggct ggagccgaac actctttact gcgtacacgt ggagtccttc 450

gtcccagggc cccctcgccg tgctcagcct tctgagaagc agtgtgccag 500

gactttgaaa gatcaatcat cagagttcaa ggctaaaatc atcttctgtt 550

atgttttgc catatctatt accgtgtttc tttttctgt gatggcttat 600

tccatctacc gatatatcca cgttggcaaa gagaaacacc cagcaaattt 650

gattttgatt tatggaaatg aatttgacaa aagattcttt gtgcctgctg 700

aaaaaaatcgt gattaacttt atcaccctca atatctcgga tgattctaaa 750

atttctcatc aggatatgag ttactggga aaaagcagtg atgtatccag 800

ccttaatgtat cctcagccca gcgggaacct gaggccccct caggaggaag 850

aggaggtgaa acattnaggg tatgcttcgc atttgatgga aattttttgt 900

gactctgaag aaaacacgga aggtacttct ctcacccagc aagagtccct 950
cagcagaaca atacccccgg ataaaacagt cattgaatat gaatatgatg 1000
tcagaaccac tgacatttgt gcggggcctg aagagcagga gctcagttg 1050
caggaggagg tgtccacaca aggaacatta ttggagtcgc aggca cggtt 1100
ggcagtcttg ggcccgcaaa cgttacagta ctcatacacc cctcagctcc 1150
aagacttaga cccctggcg caggagcaca cagactcgga ggagggccg 1200
gaggaagagc catcgacgac cctggcgac tggatcccc aaactggcag 1250
gctgtgtatt ccttcgctgt ccagcttcga ccaggattca gagggctgcg 1300
agccttctga gggggatggg ctggagagg agggcttct atctagactc 1350
tatgaggagc cggctccaga caggccacca ggagaaaaatg aaacctatct 1400
catgcaattc atggaggaat ggggttata tgtgcagatg gaaaactgat 1450
gccaacactt cctttgcct tttgttcct gtgcaaacaa gtgagtcacc 1500
ccttgatcc cagccataaa gtacctggga taaaagaatg ttttccagt 1550
ttgtcagtgt ctgtgagaat tacttatttc tttctctat tctcatagca 1600
cgtgtgtat tggttcatgc atgttaggtct cttaacaatg atggggcc 1650
tctggagtcg aggggctggc cggttgcgtt atgcagagaa agcagtcaat 1700
aaatgtttgc cagactgggt gcagaattta ttcaaggatggg tgt 1743

<210> 104
<211> 442
<212> PRT
<213> *Homo sapiens*

<400> 104
 Met Ser Tyr Asn Gly Leu His Gln Arg Val Phe Lys Glu Leu Lys
 1 5 10 15
 Leu Leu Thr Leu Cys Ser Ile Ser Ser Gln Ile Gly Pro Pro Glu
 20 25 30
 Val Ala Leu Thr Thr Asp Glu Lys Ser Ile Ser Val Val Leu Thr
 35 40 45
 Ala Pro Glu Lys Trp Lys Arg Asn Pro Glu Asp Leu Pro Val Ser
 50 55 60
 Met Gln Gln Ile Tyr Ser Asn Leu Lys Tyr Asn Val Ser Val Leu
 65 70 75
 Asn Thr Lys Ser Asn Arg Thr Trp Ser Gln Cys Val Thr Asn His
 80 85 90

Thr Leu Val Leu Thr Trp Leu Glu Pro Asn Thr Leu Tyr Cys Val
95 100 105

His Val Glu Ser Phe Val Pro Gly Pro Pro Arg Arg Ala Gln Pro
110 115 120

Ser Glu Lys Gln Cys Ala Arg Thr Leu Lys Asp Gln Ser Ser Glu
125 130 135

Phe Lys Ala Lys Ile Ile Phe Trp Tyr Val Leu Pro Ile Ser Ile
140 145 150

Thr Val Phe Leu Phe Ser Val Met Gly Tyr Ser Ile Tyr Arg Tyr
155 160 165

Ile His Val Gly Lys Glu Lys His Pro Ala Asn Leu Ile Leu Ile
170 175 180

Tyr Gly Asn Glu Phe Asp Lys Arg Phe Phe Val Pro Ala Glu Lys
185 190 195

Ile Val Ile Asn Phe Ile Thr Leu Asn Ile Ser Asp Asp Ser Lys
200 205 210

Ile Ser His Gln Asp Met Ser Leu Leu Gly Lys Ser Ser Asp Val
215 220 225

Ser Ser Leu Asn Asp Pro Gln Pro Ser Gly Asn Leu Arg Pro Pro
230 235 240

Gln Glu Glu Glu Glu Val Lys His Leu Gly Tyr Ala Ser His Leu
245 250 255

Met Glu Ile Phe Cys Asp Ser Glu Glu Asn Thr Glu Gly Thr Ser
260 265 270

Leu Thr Gln Gln Glu Ser Leu Ser Arg Thr Ile Pro Pro Asp Lys
275 280 285

Thr Val Ile Glu Tyr Glu Tyr Asp Val Arg Thr Thr Asp Ile Cys
290 295 300

Ala Gly Pro Glu Glu Gln Glu Leu Ser Leu Gln Glu Glu Val Ser
305 310 315

Thr Gln Gly Thr Leu Leu Glu Ser Gln Ala Ala Leu Ala Val Leu
320 325 330

Gly Pro Gln Thr Leu Gln Tyr Ser Tyr Thr Pro Gln Leu Gln Asp
335 340 345

Leu Asp Pro Leu Ala Gln Glu His Thr Asp Ser Glu Glu Gly Pro
350 355 360

Glu Glu Glu Pro Ser Thr Thr Leu Val Asp Trp Asp Pro Gln Thr
365 370 375

Gly Arg Leu Cys Ile Pro Ser Leu Ser Ser Phe Asp Gln Asp Ser
380 385 390
Glu Gly Cys Glu Pro Ser Glu Gly Asp Gly Leu Gly Glu Glu Gly
395 400 405
Leu Leu Ser Arg Leu Tyr Glu Glu Pro Ala Pro Asp Arg Pro Pro
410 415 420
Gly Glu Asn Glu Thr Tyr Leu Met Gln Phe Met Glu Glu Trp Gly
425 430 435
Leu Tyr Val Gln Met Glu Asn
440

<210> 105
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 105
cgctgctgct gttgctcctg g 21

<210> 106
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 106
cagtgtgcc a ggactttg 18

<210> 107
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 107
agtcgcaggc a g c g t t g g 18

<210> 108
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 108
ctcctccgag tctgtgtgct cctgc 25

<210> 109
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 109
ggacgggcag ttccctgtgt ctctgggtggt ttgcctaaac ctgcaaacat 50
c 51

<210> 110
<211> 1114
<212> DNA
<213> Homo sapiens

<400> 110
cgacgcgtg ggccggacgcg tggggcggacg cgtgggtctc tgcggggaga 50
cgccagcctg cgtctgccat ggggctcggg ttgaggggct ggggacgtcc 100
tctgctgact gtggccaccg ccctgatgct gcccgtgaag ccccccgca 150
gctcctgggg ggcccagatc atcgggggccc acgaggtgac cccccactcc 200
aggccctaca tggcatccgt ggccttcggg ggccaacatc actgcggagg 250
cttcctgctg cgagcccgct gggtggtctc ggccgcccac tgcttcagcc 300
acagagacct ccgcactggc ctgggtggc tgggcgcaca cgtcctgagt 350
actgcggagc ccacccagca ggtgtttggc atcgatgctc tcaccacgca 400
ccccgactac caccccatga cccacgc当地 cgacatctgc ctgctgcggc 450
tgaacggctc tgctgtcctg ggcctgc当地 tggggctgct gaggctgcca 500
gggagaaggg ccaggcccc cacagggggg acacggtgcc gggtggtgg 550
ctggggcttc gtgtctgact ttgaggagct gcccctggc ctgatggagg 600
ccaagggtccg agtgctggac ccggacgtct gcaacagctc ctggaaaggc 650
cacctgacac ttaccatgct ctgcacccgc agtggggaca gccacagacg 700
gggcttctgc tcggccgact ccggaggggcc cctgggtgtc aggaaccggg 750
ctcacggcct cgtttccttc tcgggcctct ggtgcggcga ccccaagacc 800
cccgacgtgt acacgcaggt gtccgcctt gtggcctggc tctggacgt 850
ggttcggcgg agcagtcccc agcccgcccc cctgc当地ggg accaccaggc 900

ccccaggaga agccgcctga gccacaacct tgcggcatgc aaatgagatg 950
gccgctccag gcctggaatg ttccgtggct gggccccacg ggaagcctga 1000
tgttcagggt tgggtggga cgggcagcgg tggggcacac ccattccaca 1050
tgcaaaggc agaagcaaac ccagtaaaat gttaactgac aaaaaaaaaa 1100
aaaaaaaaaa gaaa 1114

<210> 111
<211> 283
<212> PRT
<213> Homo sapiens

<400> 111
Met Gly Leu Gly Leu Arg Gly Trp Gly Arg Pro Leu Leu Thr Val
1 5 10 15
Ala Thr Ala Leu Met Leu Pro Val Lys Pro Pro Ala Gly Ser Trp
20 25 30
Gly Ala Gln Ile Ile Gly Gly His Glu Val Thr Pro His Ser Arg
35 40 45
Pro Tyr Met Ala Ser Val Arg Phe Gly Gly Gln His His Cys Gly
50 55 60
Gly Phe Leu Leu Arg Ala Arg Trp Val Val Ser Ala Ala His Cys
65 70 75
Phe Ser His Arg Asp Leu Arg Thr Gly Leu Val Val Leu Gly Ala
80 85 90
His Val Leu Ser Thr Ala Glu Pro Thr Gln Gln Val Phe Gly Ile
95 100 105
Asp Ala Leu Thr Thr His Pro Asp Tyr His Pro Met Thr His Ala
110 115 120
Asn Asp Ile Cys Leu Leu Arg Leu Asn Gly Ser Ala Val Leu Gly
125 130 135
Pro Ala Val Gly Leu Leu Arg Leu Pro Gly Arg Arg Ala Arg Pro
140 145 150
Pro Thr Ala Gly Thr Arg Cys Arg Val Ala Gly Trp Gly Phe Val
155 160 165
Ser Asp Phe Glu Glu Leu Pro Pro Gly Leu Met Glu Ala Lys Val
170 175 180
Arg Val Leu Asp Pro Asp Val Cys Asn Ser Ser Trp Lys Gly His
185 190 195
Leu Thr Leu Thr Met Leu Cys Thr Arg Ser Gly Asp Ser His Arg

	200	205	210											
Arg	Gly	Phe	Cys	Ser	Ala	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Arg
	215							220					225	
Asn	Arg	Ala	His	Gly	Leu	Val	Ser	Phe	Ser	Gly	Leu	Trp	Cys	Gly
	230						235					240		
Asp	Pro	Lys	Thr	Pro	Asp	Val	Tyr	Thr	Gln	Val	Ser	Ala	Phe	Val
	245							250				255		
Ala	Trp	Ile	Trp	Asp	Val	Val	Arg	Arg	Ser	Ser	Pro	Gln	Pro	Gly
	260						265					270		
Pro	Leu	Pro	Gly	Thr	Thr	Arg	Pro	Pro	Gly	Glu	Ala	Ala		
	275						280							

<210> 112
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 112
gacgtctgca acagctcctg gaag 24

<210> 113
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 113
cgagaaggaa acgaggccgt gag 23

<210> 114
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 114
tgacacttac catgctctgc acccgcatgt gggacagcca caga 44

<210> 115
<211> 1808
<212> DNA
<213> Homo sapiens

<400> 115
gagctaccca ggccggctgggt gtgcagcaag ctccgcgcgg actccggacg 50

cctgacgcct gacgcctgtc cccggcccgg catgagccgc tacctgctgc 100
cgctgtcgcc gctgggcacg gtagcaggcg ccgcgtgct gctcaaggac 150
tatgtcaccg gtggggcttg cccccagcaag gccaccatcc ctggaaagac 200
ggtcatcgtg acgggcgcca acacaggcat cggaaggcag accgccttgg 250
aactggccag gagaggaggc aacatcatcc tggcctgccc agacatggag 300
aagtgtgagg cgccagcaaa ggacatccgc gggagaccc tcaatcacca 350
tgtcaacgcc cggcacctgg acttggcttc cctcaagtct atccgagagt 400
ttcagcaaa gatcatgtaa gaggaggagc gatggacat tctaataaac 450
aacgcgggtg tggatgcggtg cccccactgg accaccgagg acggcttoga 500
gatgcagttt ggcgttaacc acctgggtca ctttctcttg acaaacttgc 550
tgctggacaa gctgaaagcc tcagcccctt cgccgatcat caacctctcg 600
tccctggccc atgttgctgg gcacatagac tttgacgact tgaactggca 650
gacgaggaag tataacacca aagccgccta ctgcccagagc aagctcgcca 700
tcgtcctctt caccaaggag ctgagccggc ggctgcaagg ctctggtg 750
actgtcaacg ccctgcaccc cggcgtggcc aggacagagc tggcagaca 800
cacgggcattc catggctcca ctttctccag caccacactc gggccatct 850
tctggctgct ggtcaagagc cccgagctgg ccgcggcagcc cagcacatac 900
ctggccgtgg cggaggaact ggcggatgtt tccggaaagt acttcgatgg 950
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ggaggcttg ggctgaaagt gcccgcctgg tgggcttaga ggctccctct 1050
gtgagggagc agccctccc cagataaccc ctggagcaga tttgaaagcc 1100
aggatggcgc ctccagaccc agacagctg tccgcctatgc ccgcagcttc 1150
ctggcactac ctgagccggg agacccaggaa ctggcggccg ccatgcccc 1200
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gcactgcccc gggctctggc tggttccgtc tgctctgctg ccagcagggg 1300
agagggggcca tctgatgctt cccctggaa tctaaactgg gaatggccga 1350
ggaggaaggg gctctgtgca ctgcaggcc acgtcaggag agccagcgg 1400
gcctgtcgcc gagggttcca aggtgctccg tgaagagcat gggcaagttg 1450

tctgacactt ggtggattct tgggtccctg tgggaccttg tgcatgcatt 1500
gtcctctctg agccttggtt tcttcagcag tgagatgctc agaataactg 1550
ctgtctccca tcatgggttg gtacagcgag ctgttgtctg gctatggcat 1600
ggctgtgccg ggggtgtttg ctgagggctt cctgtgccag agcccagcca 1650
gagagcaggt gcaggtgtca tcccgagttc aggctctgca cggcatggag 1700
tggaaacccc accagctgct gctacaggac ctgggattgc ctgggactcc 1750
cacccctcta tcaattctca tgtagtcca aactgcagac tctcaaactt 1800
gctcattt 1808

<210> 116
<211> 331
<212> PRT
<213> Homo sapiens

<400> 116
Met Ser Arg Tyr Leu Leu Pro Leu Ser Ala Leu Gly Thr Val Ala
1 5 10 15
Gly Ala Ala Val Leu Leu Lys Asp Tyr Val Thr Gly Gly Ala Cys
20 25 30
Pro Ser Lys Ala Thr Ile Pro Gly Lys Thr Val Ile Val Thr Gly
35 40 45
Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg
50 55 60
Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys
65 70 75
Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His
80 85 90
Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg
95 100 105
Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Glu Arg Val Asp Ile
110 115 120
Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr
125 130 135
Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His
140 145 150
Phe Leu Leu Thr Asn Leu Leu Asp Lys Leu Lys Ala Ser Ala
155 160 165
Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly
170 175 180

His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn
185 190 195

Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu Phe
200 205 210

Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr Val
215 220 225

Asn Ala Leu His Pro Gly Val Ala Arg Thr Glu Leu Gly Arg His
230 235 240

Thr Gly Ile His Gly Ser Thr Phe Ser Ser Thr Thr Leu Gly Pro
245 250 255

Ile Phe Trp Leu Leu Val Lys Ser Pro Glu Leu Ala Ala Gln Pro
260 265 270

Ser Thr Tyr Leu Ala Val Ala Glu Glu Leu Ala Asp Val Ser Gly
275 280 285

Lys Tyr Phe Asp Gly Leu Lys Gln Lys Ala Pro Ala Pro Glu Ala
290 295 300

Glu Asp Glu Glu Val Ala Arg Arg Leu Trp Ala Glu Ser Ala Arg
305 310 315

Leu Val Gly Leu Glu Ala Pro Ser Val Arg Glu Gln Pro Leu Pro
320 325 330

Arg

<210> 117
<211> 2249
<212> DNA
<213> Homo sapiens

<400> 117
gaagttcgcg agcgctggca tgtggtcctg gggcgccgt ggccggcgctg 50
ctggcggtgc tggcgctcgg gacaggagac ccagaaaggg ctgcggctcg 100
gggcgacacg ttctcgccgc tgaccagcgt ggcgcgcgcc ctggcgcccg 150
agcgccggct gctggggctg ctgaggcggt acctgcgcgg ggaggaggcg 200
cggtcgccgg acctgactag attctacgac aaggtaactt ctttgcatga 250
ggattcaaca acccctgtgg ctaaccctct gcttgcattt actctcatca 300
aacgcctgca gtctgactgg aggaatgtgg tacatagtct ggaggccagt 350
gagaacatcc gagctctgaa ggatggctat gagaaggtgg agcaagacct 400
tccagcctt gaggacctt gaggagcagc aaggccctg atgcggctgc 450

aggacgtgta catgctcaat gtgaaaggcc tggcccgagg tgtctttcag 500
agagtcactg gctctgccat cactgacctg tacagccccca aacggctctt 550
ttctctcaca ggggatgact gcttccaagt tggcaaggtg gcctatgaca 600
tgggggatta ttaccatgcc attccatggc tggaggaggc tgtcagtctc 650
ttccgaggat cttacggaga gtggaagaca gaggatgagg caagtctaga 700
agatgccttg gatcaacttg cctttgctta tttccggca ggaaatgttt 750
cgtgtgcctt cagcctctct cggagtttc ttctctacag cccagataat 800
aagaggatgg ccaggaatgt ctgaaaatat gaaaggctct tggcagagag 850
cccccaaccac gtggtagctg aggctgtcat ccagaggccc aatatacccc 900
acctgcagac cagagacacc tacgaggggc tatgtcagac cctgggttcc 950
cagcccactc tctaccagat ccctagcctc tactttcct atgagaccaa 1000
ttccaacgcc tacctgctgc tccagcccat ccggaaggag gtcatccacc 1050
tggagcccta cattgctctc taccatgact tcgtcagtga ctcagaggct 1100
cagaaaatta gagaacttgc agaaccatgg ctacagaggt cagtggtggc 1150
atcaggggag aagcagttac aagtggagta ccgcattcagc aaaagtgcct 1200
ggctgaagga cactgttgac ccaaaaactgg tgaccctcaa ccaccgcatt 1250
gctccctca caggccttga tgtccggctt ccctatgcag agtatctgca 1300
ggtggtaac tatggcatcg gaggacacta tgacgcctcac tttgaccatg 1350
ctacgtcacc aagcagcccc ctctacagaa tgaagtcaagg aaaccgagtt 1400
gcaacattta tgatctatct gagctcggtg gaagctggag gagccacagc 1450
cttcatctat gccaacctca gcgtgcctgt ggtaggaat gcagcactgt 1500
tttggtgaa cctgcacagg agtggtaag gggacagtga cacacttcat 1550
gctggctgtc ctgtcccttgtt gggagataag tgggtggcca acaagtggat 1600
acatgagttt ggacaggaat tccgcagacc ctgcagctcc agccctgaag 1650
actgaactgt tggcagagag aagctggtg agtcctgtgg ctttccagag 1700
aagccaggag ccaaaaagctg gggtaggaga ggagaaagca gagcagcctc 1750
ctggaagaag gccttgcag ctttgcgtgtt gcctcgcaaa tcagaggcaa 1800
gggagagggtt gttaccaggg gacactgaga atgtacattt gatctgcccc 1850

agccacggaa gtcagagtag gatgcacagt acaaaggagg ggggagtgga 1900
ggcctgagag ggaagttct ggagttcaga tactctctgt tggAACAGG 1950
acatctcaac agtctcaggt tcgatcagtg ggtctttgg cacttgAAC 2000
cttgaccaca gggaccaaga agtggcaatg aggacacctg caggagggc 2050
tagcctgact cccagaacctt taagactttc tccccactgc cttctgctgc 2100
agcccaagca gggagtgtcc ccctcccaga agcatatccc agatgagtgg 2150
tacattatat aaggatTTT tttaagttga aaacaacttt ctTTTcttt 2200
tgtatgatgg ttttttaaca cagtcattaa aaatgtttat aaatcaaaa 2249

<210> 118
<211> 544
<212> PRT
<213> Homo sapiens

<400> 118
Met Gly Pro Gly Ala Arg Leu Ala Ala Leu Leu Ala Val Leu Ala
1 5 10 15

Leu Gly Thr Gly Asp Pro Glu Arg Ala Ala Ala Arg Gly Asp Thr
20 25 30

Phe Ser Ala Leu Thr Ser Val Ala Arg Ala Leu Ala Pro Glu Arg
35 40 45

Arg Leu Leu Gly Leu Leu Arg Arg Tyr Leu Arg Gly Glu Glu Ala
50 55 60

Arg Leu Arg Asp Leu Thr Arg Phe Tyr Asp Lys Val Leu Ser Leu
65 70 75

His Glu Asp Ser Thr Thr Pro Val Ala Asn Pro Leu Leu Ala Phe
80 85 90

Thr Leu Ile Lys Arg Leu Gln Ser Asp Trp Arg Asn Val Val His
95 100 105

Ser Leu Glu Ala Ser Glu Asn Ile Arg Ala Leu Lys Asp Gly Tyr
110 115 120

Glu Lys Val Glu Gln Asp Leu Pro Ala Phe Glu Asp Leu Glu Gly
125 130 135

Ala Ala Arg Ala Leu Met Arg Leu Gln Asp Val Tyr Met Leu Asn
140 145 150

Val Lys Gly Leu Ala Arg Gly Val Phe Gln Arg Val Thr Gly Ser
155 160 165

Ala Ile Thr Asp Leu Tyr Ser Pro Lys Arg Leu Phe Ser Leu Thr
170 175 180

Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly
185 190 195

Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu
200 205 210

Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser
215 220 225

Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala
230 235 240

Gly Asn Val Ser Cys Ala Leu Ser Leu Ser Arg Glu Phe Leu Leu
245 250 255

Tyr Ser Pro Asp Asn Lys Arg Met Ala Arg Asn Val Leu Lys Tyr
260 265 270

Glu Arg Leu Leu Ala Glu Ser Pro Asn His Val Val Ala Glu Ala
275 280 285

Val Ile Gln Arg Pro Asn Ile Pro His Leu Gln Thr Arg Asp Thr
290 295 300

Tyr Glu Gly Leu Cys Gln Thr Leu Gly Ser Gln Pro Thr Leu Tyr
305 310 315

Gln Ile Pro Ser Leu Tyr Cys Ser Tyr Glu Thr Asn Ser Asn Ala
320 325 330

Tyr Leu Leu Leu Gln Pro Ile Arg Lys Glu Val Ile His Leu Glu
335 340 345

Pro Tyr Ile Ala Leu Tyr His Asp Phe Val Ser Asp Ser Glu Ala
350 355 360

Gln Lys Ile Arg Glu Leu Ala Glu Pro Trp Leu Gln Arg Ser Val
365 370 375

Val Ala Ser Gly Glu Lys Gln Leu Gln Val Glu Tyr Arg Ile Ser
380 385 390

Lys Ser Ala Trp Leu Lys Asp Thr Val Asp Pro Lys Leu Val Thr
395 400 405

Leu Asn His Arg Ile Ala Ala Leu Thr Gly Leu Asp Val Arg Pro
410 415 420

Pro Tyr Ala Glu Tyr Leu Gln Val Val Asn Tyr Gly Ile Gly Gly
425 430 435

His Tyr Glu Pro His Phe Asp His Ala Thr Ser Pro Ser Ser Pro
440 445 450

Leu Tyr Arg Met Lys Ser Gly Asn Arg Val Ala Thr Phe Met Ile
455 460 465

Tyr Leu Ser Ser Val Glu Ala Gly Gly Ala Thr Ala Phe Ile Tyr
470 475 480

Ala Asn Leu Ser Val Pro Val Val Arg Asn Ala Ala Leu Phe Trp
485 490 495

Trp Asn Leu His Arg Ser Gly Glu Gly Asp Ser Asp Thr Leu His
500 505 510

Ala Gly Cys Pro Val Leu Val Gly Asp Lys Trp Val Ala Asn Lys
515 520 525

Trp Ile His Glu Tyr Gly Gln Glu Phe Arg Arg Pro Cys Ser Ser
530 535 540

Ser Pro Glu Asp

<210> 119
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 119
cgggacagga gacccagaaa ggg 23

<210> 120
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 120
ggccaagtga tccaaaggcat cttc 24

<210> 121
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 121
ctgcgggacc tgacttagatt ctacgacaag gtactttctt tgcatgggg 49

<210> 122
<211> 1778
<212> DNA
<213> Homo sapiens

<400> 122
gagataggga gtctgggtt aagttcctgc tccatctcag gagcccctgc 50
tcccacccct aggaagccac cagactccac ggtgtggggc caatcaggtg 100
gaatcgcccc tggcaggtgg ggccacgagc gctggctgag ggaccgagcc 150
ggagagcccc ggagccccc taacccgcgc gggagcgcc cagatgccg 200
cgcggggact cgagcaggt gcgctactgc gcgcgttct cctacctctg 250
gctcaagttt tcacttatca tctattccac cgtgttctgg ctgattgggg 300
ccctggtcct gtctgtggc atctatgcag aggtttagcg gcagaaatat 350
aaaacccttg aaagtgcctt cctggctcca gccatcatcc tcatacctcct 400
gggcgtcgtc atgttcatgg tctccttcat tgggtgtgtc gcgtccctcc 450
gtgacaacct gtaccttctc caagcattca tgtacatcct tggatctgc 500
ctcatcatgg agctcattgg tggcgtggg gccttgcacct tccggaaacca 550
gaccattgac ttccctgaacg acaacattcg aagaggaatt gagaactact 600
atgatgatct ggacttcaaa aacatcatgg actttgttca gaaaaagttc 650
aagtgtgtg gcggggagga ctaccgagat tggagcaaga atcagtagcca 700
cgactgcagt gcccctggac ccctggcctg tgggtgccc tacacctgct 750
gcatcaggaa cacgacagaa gttgtcaaca ccatgtgtgg ctacaaaact 800
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caccaacgcc gtgatcatct gttcatggg caactacacc atcatggcgt 900
gcatcctcct gggcatcctg cttccccagt tcctgggggt gctgctgacg 950
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tccttgagcc tagtttttt ttacgtgatt tttgttaacat tcatttttt 1650
gtacagataa caggagttc tgactaatca aagctggtat ttccccgcat 1700
gttttattct tgcccttccc ccaaccagtt tgttaatcaa acaataaaaa 1750
catgttttgt tttgtttta aaaaaaaaa 1778

<210> 123

<211> 294

<212> PRT

<213> Homo sapiens

<400> 123

Met Pro Arg Gly Asp Ser Glu Gln Val Arg Tyr Cys Ala Arg Phe
1 5 10 15

Ser Tyr Leu Trp Leu Lys Phe Ser Leu Ile Ile Tyr Ser Thr Val
20 25 30

Phe Trp Leu Ile Gly Ala Leu Val Leu Ser Val Gly Ile Tyr Ala
35 40 45

Glu Val Glu Arg Gln Lys Tyr Lys Thr Leu Glu Ser Ala Phe Leu
50 55 60

Ala Pro Ala Ile Ile Leu Ile Leu Gly Val Val Met Phe Met
65 70 75

Val Ser Phe Ile Gly Val Leu Ala Ser Leu Arg Asp Asn Leu Tyr
80 85 90

Leu Leu Gln Ala Phe Met Tyr Ile Leu Gly Ile Cys Leu Ile Met
95 100 105

Glu Leu Ile Gly Gly Val Val Ala Leu Thr Phe Arg Asn Gln Thr
110 115 120

Ile Asp Phe Leu Asn Asp Asn Ile Arg Arg Gly Ile Glu Asn Tyr
125 130 135

Tyr Asp Asp Leu Asp Phe Lys Asn Ile Met Asp Phe Val Gln Lys
140 145 150

Lys Phe Lys Cys Cys Gly Gly Glu Asp Tyr Arg Asp Trp Ser Lys
155 160 165

Asn Gln Tyr His Asp Cys Ser Ala Pro Gly Pro Leu Ala Cys Gly

	170	175	180
Val Pro Tyr Thr Cys Cys Ile Arg Asn Thr Thr Glu Val Val Asn			
185	190		195
Thr Met Cys Gly Tyr Lys Thr Ile Asp Lys Glu Arg Phe Ser Val			
200	205		210
Gln Asp Val Ile Tyr Val Arg Gly Cys Thr Asn Ala Val Ile Ile			
215	220		225
Trp Phe Met Asp Asn Tyr Thr Ile Met Ala Cys Ile Leu Leu Gly			
230	235		240
Ile Leu Leu Pro Gln Phe Leu Gly Val Leu Leu Thr Leu Leu Tyr			
245	250		255
Ile Thr Arg Val Glu Asp Ile Ile Met Glu His Ser Val Thr Asp			
260	265		270
Gly Leu Leu Gly Pro Gly Ala Lys Pro Ser Val Glu Ala Ala Gly			
275	280		285
Thr Gly Cys Cys Leu Cys Tyr Pro Asn			
290			

<210> 124
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 124
atcatctatt ccaccgtgtt ctggc 25

<210> 125
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 125
gacagagtgc tccatgatga tgtcc 25

<210> 126
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 126

cctgtctgtg ggcatctatg cagagggttga gcggcagaaa tataaaaccc 50

<210> 127

<211> 1636

<212> DNA

<213> Homo sapiens

<400> 127

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gctgccctct gacacctggg aagatggccg gcccgtggac cttcaccctt 100

ctctgtggtt tgctggcagc caccttgatc caagccaccc tcagtcccac 150

tgcagttctc atcctcgcc caaaagtcat caaagaaaag ctgacacagg 200

agctgaagga ccacaacgcc accagcatcc tgcagcagct gccgctgctc 250

agtgcctatgc gggaaaagcc agccggaggc atccctgtgc tggcagcct 300

ggtgaacacc gtcctgaagc acatcatctg gctgaaggc atcacagcta 350

acatcctcca gctgcaggtg aagccctcg ccaatgacca ggagctgcta 400

gtcaagatcc ccctggacat ggtggctgga ttcaacacgc ccctggtaa 450

gaccatcgta gagttccaca tgacgactga gccccaaagcc accatccgca 500

tggacaccag tgcaagtggc cccacccgccc tggcctcag tgactgtgcc 550

accagccatg ggagcctgctg catccaaactg ctgtataagc tctccttcct 600

ggtgaacgcc ttagctaagc aggtcatgaa cctccttagtgc ccatccctgc 650

ccaatctagt gaaaaaccag ctgtgtcccg tgatcgaggc ttccttcaat 700

ggcatgtatg cagacccct gcagctggtg aaggtgccc tttccctcag 750

cattgaccgt ctggagtttgc accttctgtta tcctgccatc aagggtgaca 800

ccattcagct ctacctgggg gccaagttgt tggactcaca gggaaagggtg 850

accaagtggc tcaataactc tgcagcttcc ctgacaatgc ccaccctgga 900

caacatcccg ttcagcctca tcgtgagtca ggacgtggtg aaagctgcag 950

tggctgtgt gctctctcca gaagaattca tggcctgtt ggactctgtg 1000

cttcctgaga gtgccccatcg gctgaagtca agcatcgccc tgatcaatga 1050

aaaggctgca gataagctgg gatctaccca gatcgtgaag atcctaactc 1100

aggacactcc cgagttttt atagaccaag gccatgcca ggtggcccaa 1150

ctgatcgtgc tggaaagtgtt tccctccagt gaagccctcc gccctttgtt 1200

caccctggc atcgaagcca gctcggaaagc tcagtttac accaaagggtg 1250

accaacttat actcaacttg aataacatca gctctgatcg gatccagctg 1300
atgaactctg ggattggctg gttccaacct gatgttctga aaaacatcat 1350
cactgagatc atccactcca tcctgctgcc gaaccagaat ggcaaattaa 1400
gatctgggtt cccagtgtca ttggtaagg cttgggatt cgaggcagct 1450
gagtcctcac tgaccaagga tgcccttgc cttactccag ctccttgc 1500
gaaacccagc tctcctgtct cccagtgaag acttggatgg cagccatcag 1550
ggaaggctgg gtcccagctg ggagtatggg tgtgagctct atagaccatc 1600
cctctctgca atcaataaac acttgcctgt gaaaaa 1636

<210> 128

<211> 484

<212> PRT

<213> Homo sapiens

<400> 128

Met Ala Gly Pro Trp Thr Phe Thr Leu Leu Cys Gly Leu Leu Ala
1 5 10 15

Ala Thr Leu Ile Gln Ala Thr Leu Ser Pro Thr Ala Val Leu Ile
20 25 30

Leu Gly Pro Lys Val Ile Lys Glu Lys Leu Thr Gln Glu Leu Lys
35 40 45

Asp His Asn Ala Thr Ser Ile Leu Gln Gln Leu Pro Leu Leu Ser
50 55 60

Ala Met Arg Glu Lys Pro Ala Gly Gly Ile Pro Val Leu Gly Ser
65 70 75

Leu Val Asn Thr Val Leu Lys His Ile Ile Trp Leu Lys Val Ile
80 85 90

Thr Ala Asn Ile Leu Gln Leu Gln Val Lys Pro Ser Ala Asn Asp
95 100 105

Gln Glu Leu Leu Val Lys Ile Pro Leu Asp Met Val Ala Gly Phe
110 115 120

Asn Thr Pro Leu Val Lys Thr Ile Val Glu Phe His Met Thr Thr
125 130 135

Glu Ala Gln Ala Thr Ile Arg Met Asp Thr Ser Ala Ser Gly Pro
140 145 150

Thr Arg Leu Val Leu Ser Asp Cys Ala Thr Ser His Gly Ser Leu
155 160 165

Arg Ile Gln Leu Leu Tyr Lys Leu Ser Phe Leu Val Asn Ala Leu

	170	175	180
Ala Lys Gln Val Met Asn Leu Leu Val Pro Ser Leu Pro Asn Leu			
185	190	195	
Val Lys Asn Gln Leu Cys Pro Val Ile Glu Ala Ser Phe Asn Gly			
200	205	210	
Met Tyr Ala Asp Leu Leu Gln Leu Val Lys Val Pro Ile Ser Leu			
215	220	225	
Ser Ile Asp Arg Leu Glu Phe Asp Leu Leu Tyr Pro Ala Ile Lys			
230	235	240	
Gly Asp Thr Ile Gln Leu Tyr Leu Gly Ala Lys Leu Leu Asp Ser			
245	250	255	
Gln Gly Lys Val Thr Lys Trp Phe Asn Asn Ser Ala Ala Ser Leu			
260	265	270	
Thr Met Pro Thr Leu Asp Asn Ile Pro Phe Ser Leu Ile Val Ser			
275	280	285	
Gln Asp Val Val Lys Ala Ala Val Ala Ala Val Leu Ser Pro Glu			
290	295	300	
Glu Phe Met Val Leu Leu Asp Ser Val Leu Pro Glu Ser Ala His			
305	310	315	
Arg Leu Lys Ser Ser Ile Gly Leu Ile Asn Glu Lys Ala Ala Asp			
320	325	330	
Lys Leu Gly Ser Thr Gln Ile Val Lys Ile Leu Thr Gln Asp Thr			
335	340	345	
Pro Glu Phe Phe Ile Asp Gln Gly His Ala Lys Val Ala Gln Leu			
350	355	360	
Ile Val Leu Glu Val Phe Pro Ser Ser Glu Ala Leu Arg Pro Leu			
365	370	375	
Phe Thr Leu Gly Ile Glu Ala Ser Ser Glu Ala Gln Phe Tyr Thr			
380	385	390	
Lys Gly Asp Gln Leu Ile Leu Asn Leu Asn Asn Ile Ser Ser Asp			
395	400	405	
Arg Ile Gln Leu Met Asn Ser Gly Ile Gly Trp Phe Gln Pro Asp			
410	415	420	
Val Leu Lys Asn Ile Ile Thr Glu Ile Ile His Ser Ile Leu Leu			
425	430	435	
Pro Asn Gln Asn Gly Lys Leu Arg Ser Gly Val Pro Val Ser Leu			
440	445	450	
Val Lys Ala Leu Gly Phe Glu Ala Ala Glu Ser Ser Leu Thr Lys			

455

460

465

Asp Ala Leu Val Leu Thr Pro Ala Ser Leu Trp Lys Pro Ser Ser
470 475 480

Pro Val Ser Gln

<210> 129

<211> 2213

<212> DNA

<213> Homo sapiens

<400> 129

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aaagaaggag atggtgttat ctgaaaaggt tagtcagctg atggaatgga 150

ctaacaaaag acctgtataa agaatgaatg gagacaagtt ccgtcgccct 200

tgaaaaagccc caccgagaaaa ttactccgtt atcgtcatgt tcactgctct 250

ccaactgcat agacagtgtg tcgtttgcaa gcaagctgat gaagaattcc 300

agatcctggc aaactcctgg cgatactcca gtgcattcac caacaggata 350

tttttgcca tggtgattt tggatggc tctgatgtat ttcatgtct 400

aaacatgaat tcagctccaa ctttcataa ctttcctgca aaaggaaac 450

ccaaacgggg tgatacatat gagttacagg tgcgggtttt ttcatgtct 500

cagattgccc ggtggatcgc cgacagaact gatgtcaata ttagagtat 550

tagaccccca aattatgctg gtcccttat gttggattt cttttggctg 600

ttattgggg acttggatgtat cttcgaagaa gtaatatgga atttctcttt 650

aataaaaactg gatgggcttt tgcagcttg tgtttggc ttgctatgac 700

atctggtaa atgtggaaacc atataagagg accaccatat gcccataaga 750

atccccacac gggacatgtg aattatatcc atggaagcag tcaagcccag 800

ttttagctg aaacacacat ttttcttctg ttatgggtg gagttacctt 850

aggaatgggtg ctttatgtg aagctgctac ctctgacatg gatattggaa 900

agcgaaagat aatgtgtgtg gctggattt gacttggatg attattcttc 950

agttggatgc tctctatgtt tagatctaaa tatcatggct acccatacag 1000

ctttctgtatg agttaaaaag gtcccagaga tatatagaca ctggagtact 1050

ggaaattgaa aaacgaaaat cgtgtgtgtt tgaaaagaag aatgcaactt 1100

gtatattttg tattacctct tttttcaag tgatttaaat agttaatcat 1150
ttaaccaaag aagatgtgta gtgccttaac aagcaatcct ctgtcaaaat 1200
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aactactact ttgttttagt tagaacaaag ctcaaaacta cttagttaa 1350
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agatcacgccc actgcactcc agcctggcaa cagagcgaga ctccatctca 2200
aaaaaaaaaa aaa 2213

<210> 130
<211> 335
<212> PRT
<213> Homo sapiens

<400> 130
Met Ala Ala Arg Trp Arg Phe Trp Cys Val Ser Val Thr Met Val
1 5 10 15
Val Ala Leu Leu Ile Val Cys Asp Val Pro Ser Ala Ser Ala Gln

	20	25	30
Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met			
35	40	45	
Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys			
50	55	60	
Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile			
65	70	75	
Val Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys			
80	85	90	
Lys Gln Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg			
95	100	105	
Tyr Ser Ser Ala Phe Thr Asn Arg Ile Phe Phe Ala Met Val Asp			
110	115	120	
Phe Asp Glu Gly Ser Asp Val Phe Gln Met Leu Asn Met Asn Ser			
125	130	135	
Ala Pro Thr Phe Ile Asn Phe Pro Ala Lys Gly Lys Pro Lys Arg			
140	145	150	
Gly Asp Thr Tyr Glu Leu Gln Val Arg Gly Phe Ser Ala Glu Gln			
155	160	165	
Ile Ala Arg Trp Ile Ala Asp Arg Thr Asp Val Asn Ile Arg Val			
170	175	180	
Ile Arg Pro Pro Asn Tyr Ala Gly Pro Leu Met Leu Gly Leu Leu			
185	190	195	
Leu Ala Val Ile Gly Gly Leu Val Tyr Leu Arg Arg Ser Asn Met			
200	205	210	
Glu Phe Leu Phe Asn Lys Thr Gly Trp Ala Phe Ala Ala Leu Cys			
215	220	225	
Phe Val Leu Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg			
230	235	240	
Gly Pro Pro Tyr Ala His Lys Asn Pro His Thr Gly His Val Asn			
245	250	255	
Tyr Ile His Gly Ser Ser Gln Ala Gln Phe Val Ala Glu Thr His			
260	265	270	
Ile Val Leu Leu Phe Asn Gly Gly Val Thr Leu Gly Met Val Leu			
275	280	285	
Leu Cys Glu Ala Ala Thr Ser Asp Met Asp Ile Gly Lys Arg Lys			
290	295	300	
Ile Met Cys Val Ala Gly Ile Gly Leu Val Val Leu Phe Phe Ser			

305

310

315

Trp Met Leu Ser Ile Phe Arg Ser Lys Tyr His Gly Tyr Pro Tyr
320 325 330

Ser Phe Leu Met Ser
335

<210> 131

<211> 2476

<212> DNA

<213> Homo sapiens

<400> 131

aagcaaccaa actgcaagct ttgggagttt ttcgtgtcc ctgccctgct 50

ctgctaggga gagaacgcca gagggaggcg gctggcccg cgccaggctc 100

tcagaaccgc taccggcgat gctactgctg tgggtgtcgg tggtcgcagc 150

cttggcgctg gcggtaactgg ccccccggagc aggggagcag aggccggagag 200

cagccaaagc gcccaatgtg gtgctggctg tgaggcactc ctgcgtatgga 250

aggtaacat ttcatccagg aagtcaaggta gtgaaacttc cttttatcaa 300

cttttatgaag acacgtggga ctccctttct gaatgcctac acaaactctc 350

caatttgttg cccatcacgc gcagcaatgt ggagtggcct ctcaactcac 400

ttaacagaat ctggaaataa ttttaagggt ctagatccaa attataacaac 450

atggatggat gtcatggaga ggcattggcta ccgaacacag aaatttggga 500

aactggacta tacttcagga catcaactcca ttagtaatcg tgtggaaagcg 550

tggacaagag atgttgctt cttaactcaga caagaaggca gccccatgg 600

taatcttatac cgtaacacagga ctaaagtcaag agtgatggaa agggattggc 650

agaatacaga caaagcagta aactggtaa gaaaggaagc aattaattac 700

actgaaccat ttgttattta ctgggattta aatttaccac acccttaccc 750

ttcaccatct tctggagaaa attttggatc ttcaacattt cacacatctc 800

tttattggct tgaaaaagtg tctcatgatg ccatcaaat cccaaagtgg 850

tcacctttgt cagaaatgca ccctgttagat tattactctt cttataacaa 900

aaactgcact ggaagattta caaaaaaaga aattaagaat attagagcat 950

tttattatgc tatgtgtgct gagacagatg ccatgcttgg tgaaattatt 1000

ttggcccttc atcaattaga tcttcttcag aaaactattg tcataactc 1050

ctcagaccat ggagagctgg ccatggaca tcgacagttt tataaaatga 1100

gcatgtacga ggctagtgca catgttccgc ttttcatatgat gggaccaggaa 1150
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ccctaccatg cttgatattg ctggattcc tctgcctcag aacctgagtg 1250
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tgtgaatgcc tccacctaca tgcttcgaac taaccactgg aaatatata 1400
cctattcggaa tggtgcatca atattgcctc aactcttgc tcttcctcg 1450
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cttctgtcca ccagtataat aaagagcagt ttatcaagt gaaacaaagt 1600
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acctgtataatc ccaggacttt gggaggctga ggaaagcaga tcacaaggc 1900
aagagattga gaccatcctg gccaacatgg tgaaaccctg tctctactaa 1950
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tgtgtcgcaaa aaaaataaaaa ataaaataat aataattacc aatttttcat 2150
tatTTTGTAA gaatgttagt gttttaaga taaaatgcca atgattataa 2200
aatcacatat tttcaaaaat gtttattttaggccttgc tacaatttct 2250
aacaatttag tggaagtatc aaaaggattt aagcaatac tgtaacagtt 2300
atgttccttt aaataataga gaatataaaaa tattgtataa atatgtatca 2350
taaaaatagtt gtatgtgagc atttgcgtt gaaaaaaaaaaaaaaaa 2400
aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa 2450
aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaa 2476

<210> 132
<211> 536
<212> PRT
<213> Homo sapiens

<400> 132
Met Leu Leu Leu Trp Val Ser Val Val Ala Ala Leu Ala Leu Ala
1 5 10 15

Val Leu Ala Pro Gly Ala Gly Glu Gln Arg Arg Arg Ala Ala Lys
20 25 30

Ala Pro Asn Val Val Leu Val Val Ser Asp Ser Phe Asp Gly Arg
35 40 45

Leu Thr Phe His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile
50 55 60

Asn Phe Met Lys Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr
65 70 75

Asn Ser Pro Ile Cys Cys Pro Ser Arg Ala Ala Met Trp Ser Gly
80 85 90

Leu Phe Thr His Leu Thr Glu Ser Trp Asn Asn Phe Lys Gly Leu.
95 100 105

Asp Pro Asn Tyr Thr Trp Met Asp Val Met Glu Arg His Gly
110 115 120

Tyr Arg Thr Gln Lys Phe Gly Lys Leu Asp Tyr Thr Ser Gly His
125 130 135

His Ser Ile Ser Asn Arg Val Glu Ala Trp Thr Arg Asp Val Ala
140 145 150

Phe Leu Leu Arg Gln Glu Gly Arg Pro Met Val Asn Leu Ile Arg
155 160 165

Asn Arg Thr Lys Val Arg Val Met Glu Arg Asp Trp Gln Asn Thr
170 175 180

Asp Lys Ala Val Asn Trp Leu Arg Lys Glu Ala Ile Asn Tyr Thr
185 190 195

Glu Pro Phe Val Ile Tyr Leu Gly Leu Asn Leu Pro His Pro Tyr
200 205 210

Pro Ser Pro Ser Ser Gly Glu Asn Phe Gly Ser Ser Thr Phe His
215 220 225

Thr Ser Leu Tyr Trp Leu Glu Lys Val Ser His Asp Ala Ile Lys
230 235 240

Ile Pro Lys Trp Ser Pro Leu Ser Glu Met His Pro Val Asp Tyr
245 250 255

Tyr Ser Ser Tyr Thr Lys Asn Cys Thr Gly Arg Phe Thr Lys Lys
260 265 270

Glu Ile Lys Asn Ile Arg Ala Phe Tyr Tyr Ala Met Cys Ala Glu
275 280 285

Thr Asp Ala Met Leu Gly Glu Ile Ile Leu Ala Leu His Gln Leu
290 295 300

Asp Leu Leu Gln Lys Thr Ile Val Ile Tyr Ser Ser Asp His Gly
305 310 315

Glu Leu Ala Met Glu His Arg Gln Phe Tyr Lys Met Ser Met Tyr
320 325 330

Glu Ala Ser Ala His Val Pro Leu Leu Met Met Gly Pro Gly Ile
335 340 345

Lys Ala Gly Leu Gln Val Ser Asn Val Val Ser Leu Val Asp Ile
350 355 360

Tyr Pro Thr Met Leu Asp Ile Ala Gly Ile Pro Leu Pro Gln Asn
365 370 375

Leu Ser Gly Tyr Ser Leu Leu Pro Leu Ser Ser Glu Thr Phe Lys
380 385 390

Asn Glu His Lys Val Lys Asn Leu His Pro Pro Trp Ile Leu Ser
395 400 405

Glu Phe His Gly Cys Asn Val Asn Ala Ser Thr Tyr Met Leu Arg
410 415 420

Thr Asn His Trp Lys Tyr Ile Ala Tyr Ser Asp Gly Ala Ser Ile
425 430 435

Leu Pro Gln Leu Phe Asp Leu Ser Ser Asp Pro Asp Glu Leu Thr
440 445 450

Asn Val Ala Val Lys Phe Pro Glu Ile Thr Tyr Ser Leu Asp Gln
455 460 465

Lys Leu His Ser Ile Ile Asn Tyr Pro Lys Val Ser Ala Ser Val
470 475 480

His Gln Tyr Asn Lys Glu Gln Phe Ile Lys Trp Lys Gln Ser Ile
485 490 495

Gly Gln Asn Tyr Ser Asn Val Ile Ala Asn Leu Arg Trp His Gln
500 505 510

Asp Trp Gln Lys Glu Pro Arg Lys Tyr Glu Asn Ala Ile Asp Gln
515 520 525

Trp Leu Lys Thr His Met Asn Pro Arg Ala Val
530 535

<210> 133
<211> 1475
<212> DNA
<213> Homo sapiens

<400> 133
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gcctgcatta tctctgttgt gggcatgaga tgcacagtct tctgccagga 450
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<210> 134
<211> 230
<212> PRT
<213> Homo sapiens

<400> 134
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Leu Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp
20 25 30
Lys Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly
35 40 45
Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly
50 55 60
Ile Thr Gln Cys Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala
65 70 75
Asp Ile Gln Ala Ala Gln Ala Met Met Val Thr Ser Ser Ala Ile
80 85 90
Ser Ser Leu Ala Cys Ile Ile Ser Val Val Gly Met Arg Cys Thr
95 100 105
Val Phe Cys Gln Glu Ser Arg Ala Lys Asp Arg Val Ala Val Ala
110 115 120
Gly Gly Val Phe Phe Ile Leu Gly Gly Leu Leu Gly Phe Ile Pro
125 130 135
Val Ala Trp Asn Leu His Gly Ile Leu Arg Asp Phe Tyr Ser Pro
140 145 150
Leu Val Pro Asp Ser Met Lys Phe Glu Ile Gly Glu Ala Leu Tyr
155 160 165
Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile Ala Gly Ile Ile
170 175 180
Leu Cys Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser Asn Tyr Tyr
185 190 195
Asp Ala Tyr Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser Pro Arg
200 205 210

Pro Gly Gln Pro Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr Ser
215 220 225

Leu Thr Gly Tyr Val
230

{ <210> 135

<211> 610

<212> DNA

<213> Homo sapiens

<400> 135

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aagtcatcgc tcccgtggc tcagaaccat ggctgtgcca gccggcaccc 150

aggtgtggag acaagatcta caaccccttg gagcagtgtct gttacaatga 200

cgcacatcgtg tccctgagcg agacccgcca atgtggtccc ccctgcacct 250

tctggccctg ctggagctc tgctgtcttg attcctttgg cctcacaaac 300

gattttgttg tgaagctgaa gggtcagggt gtgaattccc agtgcactc 350

atctcccatc tccagtaaat gtgaaaggcag aagacgtttt ccctgagaag 400

acatagaaag aaaatcaact ttcaactaagg catctcagaa acataggcta 450

aggttaatatg tgtaccagta gagaagcctg aggaatttac aaaatgatgc 500

agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550

atgacagtag attatcagga aataaaataaaa gtggttttc caatgtacac 600

acctgtaaaa 610

<210> 136

<211> 119

<212> PRT

<213> Homo sapiens

<400> 136

Met Val Pro Arg Ile Phe Ala Pro Ala Tyr Val Ser Val Cys Leu
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Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu
20 25 30

Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr
35 40 45

Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu
50 55 60

Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys

65 70 75

Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe
80 85 90

Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser
95 100 105

Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro
110 115

<210> 137

<211> 771

<212> DNA

<213> Homo sapiens

<400> 137

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gtggggacaa gttctacgac cccctgcagc actgttgcta tggatgtgcc 200

gtcgtgcctt tggccaggac ccagacgtgt ggaaactgca ctttcagagt 250

ctgcttgag cagtgctgcc cctggacatt catggtaag ctgataaacc 300

agaactgcga ctcagccgg acctcgatg acaggcttg tcgcagtgtc 350

agctaatttga acatcaggaa aacgatgact cctggattct ctttcctggg 400

tgggccttggaa gaaagaggct ggtgttacct gagatctggg atgctgagtg 450

gctgtttggg ggccagagaa acacacactc aactgcccac ttcattctgt 500

gacctgtctg aggcccaccc tgcagctgcc ctgaggaggc ccacaggtcc 550

ccttctagaa ttctggacag catgagatgc gtgtgctgat gggggccca 600

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accccaaggc tggctgggaa acccttcacc cttctgtgag attttccatc 700

atctcaagtt ctcttctatc caggagcaaa gcacaggatc ataataaatt 750

tatgtacttt ataaatgaaa a 771

<210> 138

<211> 110

<212> PRT

<213> Homo sapiens

<400> 138

Met Ala Pro Arg Gly Cys Ile Val Ala Val Phe Ala Ile Phe Cys

1

5

10

15

Ile Ser Arg Leu Leu Cys Ser His Gly Ala Pro Val Ala Pro Met
20 25 30

Thr Pro Tyr Leu Met Leu Cys Gln Pro His Lys Arg Cys Gly Asp
35 40 45

Lys Phe Tyr Asp Pro Leu Gln His Cys Cys Tyr Asp Asp Ala Val
50 55 60

Val Pro Leu Ala Arg Thr Gln Thr Cys Gly Asn Cys Thr Phe Arg
65 70 75

Val Cys Phe Glu Gln Cys Cys Pro Trp Thr Phe Met Val Lys Leu
80 85 90

Ile Asn Gln Asn Cys Asp Ser Ala Arg Thr Ser Asp Asp Arg Leu
95 100 105

Cys Arg Ser Val Ser
110

<210> 139

<211> 2044

<212> DNA

<213> Homo sapiens

<400> 139

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ctccccggca ccagaagttc ctctgcgcgt ccgacggcga catgggcgtc 150

cccacggccc tggaggccgg cagctggcgc tggggatccc tgctttcgc 200

tctttcctg gctgcgtccc taggtccggt ggcagcattc aaggtcgcca 250

cgcgttattc cctgtatgtc tgtcccgagg ggcagaacgt caccctcacc 300

tgcaggctct tggccctgt ggacaaaggg cacgatgtga cttctacaa 350

gacgtggta cgcagctcga gggcgaggt gcagacctgc tcagagcgcc 400

ggcccatccg caacccatcg ttccaggacc ttcacctgca ccatggaggc 450

caccaggctg ccaacaccag ccacgacctg gtcagcgcc acgggctgga 500

gtcggcctcc gaccaccatg gcaacttctc catcaccatg cgcaacctga 550

ccctgctgga tagcggcctc tactgctgcc tggtggtgga gatcaggcac 600

caccactcg agcacagggt ccatggtgcc atggagctgc aggtgcagac 650

aggcaaagat gcaccatcca actgtgtggt gtaccatcc tcctcccagg 700

atagtaaaa catcacggct gcagccctgg ctacgggtgc ctgcatacgta 750

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tggggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaga 2044

<210> 140
<211> 311
<212> PRT
<213> Homo sapiens

<400> 140

Met Gly Val Pro Thr Ala Leu Glu Ala Gly Ser Trp Arg Trp Gly
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Ser Leu Leu Phe Ala Leu Phe Leu Ala Ala Ser Leu Gly Pro Val
20 25 30

Ala Ala Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro
35 40 45

Glu Gly Gln Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val
50 55 60

Asp Lys Gly His Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser
65 70 75

Ser Arg Gly Glu Val Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg
80 85 90

Asn Leu Thr Phe Gln Asp Leu His Leu His His Gly Gly His Gln
95 100 105

Ala Ala Asn Thr Ser His Asp Leu Ala Gln Arg His Gly Leu Glu
110 115 120

Ser Ala Ser Asp His His Gly Asn Phe Ser Ile Thr Met Arg Asn
125 130 135

Leu Thr Leu Leu Asp Ser Gly Leu Tyr Cys Cys Leu Val Val Glu
140 145 150

Ile Arg His His His Ser Glu His Arg Val His Gly Ala Met Glu
155 160 165

Leu Gln Val Gln Thr Gly Lys Asp Ala Pro Ser Asn Cys Val Val
170 175 180

Tyr Pro Ser Ser Ser Gln Asp Ser Glu Asn Ile Thr Ala Ala Ala
185 190 195

Leu Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys Leu Pro Leu
200 205 210

Ile Leu Leu Leu Val Tyr Lys Gln Arg Gln Ala Ala Ser Asn Arg
215 220 225

Arg Ala Gln Glu Leu Val Arg Met Asp Ser Asn Ile Gln Gly Ile
230 235 240

Glu Asn Pro Gly Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro
245 250 255

Glu Ala Lys Val Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln
260 265 270

Pro Ser Glu Ser Gly Arg His Leu Leu Ser Glu Pro Ser Thr Pro

275 280 285

Leu Ser Pro Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp
290 295 300

Pro Val Pro Asp Ser Pro Asn Phe Glu Val Ile
305 310

<210> 141

<211> 1732

<212> DNA

<213> Homo sapiens

<400> 141

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cattaccCTC aaaaaaaaaa aaaaaaaaaa aa 1732

<210> 142
<211> 451
<212> PRT
<213> Homo sapiens

<400> 142
Met Val Pro Glu Val Arg Val Leu Ser Ser Leu Leu Gly Leu Ala
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Leu Leu Trp Phe Pro Leu Asp Ser His Ala Arg Ala Arg Pro Asp
20 25 30

Met Phe Cys Leu Phe His Gly Lys Arg Tyr Ser Pro Gly Glu Ser
35 40 45

Trp His Pro Tyr Leu Glu Pro Gln Gly Leu Met Tyr Cys Leu Arg
50 55 60

Cys Thr Cys Ser Glu Gly Ala His Val Ser Cys Tyr Arg Leu His
65 70 75

Cys Pro Pro Val His Cys Pro Gln Pro Val Thr Glu Pro Gln Gln
80 85 90

Cys Cys Pro Lys Cys Val Glu Pro His Thr Pro Ser Gly Leu Arg
95 100 105

Ala Pro Pro Lys Ser Cys Gln His Asn Gly Thr Met Tyr Gln His
110 115 120

Gly Glu Ile Phe Ser Ala His Glu Leu Phe Pro Ser Arg Leu Pro
125 130 135

Asn Gln Cys Val Leu Cys Ser Cys Thr Glu Gly Gln Ile Tyr Cys
140 145 150

Gly Leu Thr Thr Cys Pro Glu Pro Gly Cys Pro Ala Pro Leu Pro
155 160 165

Leu Pro Asp Ser Cys Cys Gln Ala Cys Lys Asp Glu Ala Ser Glu
170 175 180

Gln Ser Asp Glu Glu Asp Ser Val Gln Ser Leu His Gly Val Arg
185 190 195

His Pro Gln Asp Pro Cys Ser Ser Asp Ala Gly Arg Lys Arg Gly
200 205 210

Pro Gly Thr Pro Ala Pro Thr Gly Leu Ser Ala Pro Leu Ser Phe
215 220 225

Ile Pro Arg His Phe Arg Pro Lys Gly Ala Gly Ser Thr Thr Val
230 235 240

Lys Ile Val Leu Lys Glu Lys His Lys Lys Ala Cys Val His Gly
245 250 255

Gly Lys Thr Tyr Ser His Gly Glu Val Trp His Pro Ala Phe Arg
260 265 270

Ala Phe Gly Pro Leu Pro Cys Ile Leu Cys Thr Cys Glu Asp Gly
275 280 285

Arg Gln Asp Cys Gln Arg Val Thr Cys Pro Thr Glu Tyr Pro Cys
290 295 300

Arg His Pro Glu Lys Val Ala Gly Lys Cys Cys Lys Ile Cys Pro
305 310 315

Glu Asp Lys Ala Asp Pro Gly His Ser Glu Ile Ser Ser Thr Arg
320 325 330

Cys Pro Lys Ala Pro Gly Arg Val Leu Val His Thr Ser Val Ser
335 340 345

Pro Ser Pro Asp Asn Leu Arg Arg Phe Ala Leu Glu His Glu Ala
350 355 360

Ser Asp Leu Val Glu Ile Tyr Leu Trp Lys Leu Val Lys Asp Glu
365 370 375

Glu Thr Glu Ala Gln Arg Gly Glu Val Pro Gly Pro Arg Pro His
380 385 390

Ser Gln Asn Leu Pro Leu Asp Ser Asp Gln Glu Ser Gln Glu Ala
395 400 405

Arg Leu Pro Glu Arg Gly Thr Ala Leu Pro Thr Ala Arg Trp Pro
410 415 420

Pro Arg Arg Ser Leu Glu Arg Leu Pro Ser Pro Asp Pro Gly Ala
425 430 435

Glu Gly His Gly Gln Ser Arg Gln Ser Asp Gln Asp Ile Thr Lys
440 445 450

Thr

<210> 143

<211> 693

<212> DNA

<213> Homo sapiens

<400> 143

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cttgcggaaa atgctgatct cagtcgcaat gctggcgca ggggctggcg 150
tgggctacgc gtcctcggtt atcgtgaccc cggagagcgc gcggaagcag 200
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aactgaaaga accaataaaa tcatgttcct caaaaaaaaaaaaaaa 650
aaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaa 693

<210> 144

<211> 93

<212> PRT

<213> Homo sapiens

<400> 144

Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly
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Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro
20 25 30

Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln
35 40 45

Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu
50 55 60

Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala
65 70 75

Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Ala Ser Gly
80 85 90

Arg Ser Pro

<210> 145

<211> 1883

<212> DNA

<213> Homo sapiens

<400> 145

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atggtcggga cccctccaag gacagcagca ccaccttgc gagtacatgg 200

aacgcccact agctgcttta gaggaacggc tggcccaatgc ccaggaccag 250

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acaccatctc cgggagagtg gatcgtctgg agcgggaggt agactatctg 400

gagacccaga acccagcttgc gccctgtgtc gagtttgcgatc agaaggtgac 450

tggaggccct gggaccaaag gcaaggaaag aaggaatgag aagtacgata 500

tggtagacaga ctgtggctac acaatctctc aagttagatc aatgaagatt 550

ctgaagcgat ttgggtggcc agctggtcta tggaccaagg atccactggg 600

gcaaacagag aagatctacg tggtagatgg gacacagaat gacacagcct 650

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atatggtggc ttttttattt ttgctcggag gcctcctggc agacctggc 800

gaggtggta gatggagaac actttgcagc taatcaaatt ccacctggc 850

aaccgaacag tggtagacag ctcagtttc ccagcagagg ggctgatccc 900

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aaaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850
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<210> 146
<211> 406
<212> PRT
<213> Homo sapiens

<400> 146
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35 40 45
Asp Gln Ser Ser Arg His Ala Ala Glu Leu Arg Asp Phe Lys Asn

50 55 60
Lys Met Leu Pro Leu Leu Glu Val Ala Glu Lys Glu Arg Glu Ala
65 70 75
Leu Arg Thr Glu Ala Asp Thr Ile Ser Gly Arg Val Asp Arg Leu
80 85 90
Glu Arg Glu Val Asp Tyr Leu Glu Thr Gln Asn Pro Ala Leu Pro
95 100 105
Cys Val Glu Phe Asp Glu Lys Val Thr Gly Gly Pro Gly Thr Lys
110 115 120
Gly Lys Gly Arg Arg Asn Glu Lys Tyr Asp Met Val Thr Asp Cys
125 130 135
Gly Tyr Thr Ile Ser Gln Val Arg Ser Met Lys Ile Leu Lys Arg
140 145 150
Phe Gly Gly Pro Ala Gly Leu Trp Thr Lys Asp Pro Leu Gly Gln
155 160 165
Thr Glu Lys Ile Tyr Val Leu Asp Gly Thr Gln Asn Asp Thr Ala
170 175 180
Phe Val Phe Pro Arg Leu Arg Asp Phe Thr Leu Ala Met Ala Ala
185 190 195
Arg Lys Ala Ser Arg Val Arg Val Pro Phe Pro Trp Val Gly Thr
200 205 210
Gly Gln Leu Val Tyr Gly Gly Phe Leu Tyr Phe Ala Arg Arg Pro
215 220 225
Pro Gly Arg Pro Gly Gly Gly Glu Met Glu Asn Thr Leu Gln
230 235 240
Leu Ile Lys Phe His Leu Ala Asn Arg Thr Val Val Asp Ser Ser
245 250 255
Val Phe Pro Ala Glu Gly Leu Ile Pro Pro Tyr Gly Leu Thr Ala
260 265 270
Asp Thr Tyr Ile Asp Leu Val Ala Asp Glu Glu Gly Leu Trp Ala
275 280 285
Val Tyr Ala Thr Arg Glu Asp Asp Arg His Leu Cys Leu Ala Lys
290 295 300
Leu Asp Pro Gln Thr Leu Asp Thr Glu Gln Gln Trp Asp Thr Pro
305 310 315
Cys Pro Arg Glu Asn Ala Glu Ala Ala Phe Val Ile Cys Gly Thr
320 325 330
Leu Tyr Val Val Tyr Asn Thr Arg Pro Ala Ser Arg Ala Arg Ile

335	340	345
Gln Cys Ser Phe Asp Ala Ser Gly Thr Leu Thr Pro Glu Arg Ala		
350	355	360
Ala Leu Pro Tyr Phe Pro Arg Arg Tyr Gly Ala His Ala Ser Leu		
365	370	375
Arg Tyr Asn Pro Arg Glu Arg Gln Leu Tyr Ala Trp Asp Asp Gly		
380	385	390
Tyr Gln Ile Val Tyr Lys Leu Glu Met Arg Lys Lys Glu Glu Glu		
395	400	405
Val		

<210> 147
<211> 2052
<212> DNA
<213> Homo sapiens

<400> 147
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gttctcctct tctctcta at ccatccgtca cctctcctgt catccgttcc 150
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ttggttctga gtctcctcaa gctgggatca gggcagtggc aggtgtttgg 250
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gttcctgtc tcctaagacc aatgcagagg ccatggaagt gcgggttctc 350
agggggccagt tctctagcgt ggtccacctc tacaggacg ggaaggacca 400
gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtaagg 450
attctattgc ggaggggcgc atctctctga ggctggaaaa cattacttg 500
ttggatgctg gcctctatgg gtgcaggatt agttcccagt cttactacca 550
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tccatgcggc atgctcatct gagccgagag gtggaatcca gggtacagat 850

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gagatttaca aggaagagtg tggggcttc tcagagttc caagcaggg 1200
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cattacattt agtttgctct cactccatct ggctaagtga tcttgaata 1900
ccacccctca ggtgaagaac cgtaggaat tcccatctca caggctgtgg 1950
tgttagattaa gtagacaagg aatgtgaata atgcttagat cttattgatg 2000
acagagtgtta tcctaattggg ttgttcatta tattacactt tcagtaaaaa 2050
aa 2052

<210> 148
<211> 500
<212> PRT
<213> Homo sapiens

<400> 148
Met Ala Leu Met Leu Ser Leu Val Leu Ser Leu Leu Lys Leu Gly

~

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			20			25								30	
Leu	Val	Gly	Glu	Asp	Ala	Ala	Phe	Ser	Cys	Phe	Leu	Ser	Pro	Lys	
			35				40							45	
Thr	Asn	Ala	Glu	Ala	Met	Glu	Val	Arg	Phe	Phe	Arg	Gly	Gln	Phe	
			50			55								60	
Ser	Ser	Val	Val	His	Leu	Tyr	Arg	Asp	Gly	Lys	Asp	Gln	Pro	Phe	
			65			70								75	
Met	Gln	Met	Pro	Gln	Tyr	Gln	Gly	Arg	Thr	Lys	Leu	Val	Lys	Asp	
			80			85								90	
Ser	Ile	Ala	Glu	Gly	Arg	Ile	Ser	Leu	Arg	Leu	Glu	Asn	Ile	Thr	
			95				100							105	
Val	Leu	Asp	Ala	Gly	Leu	Tyr	Gly	Cys	Arg	Ile	Ser	Ser	Gln	Ser	
			110			115								120	
Tyr	Tyr	Gln	Lys	Ala	Ile	Trp	Glu	Leu	Gln	Val	Ser	Ala	Leu	Gly	
			125			130								135	
Ser	Val	Pro	Leu	Ile	Ser	Ile	Thr	Gly	Tyr	Val	Asp	Arg	Asp	Ile	
			140			145								150	
Gln	Leu	Leu	Cys	Gln	Ser	Ser	Gly	Trp	Phe	Pro	Arg	Pro	Thr	Ala	
			155			160								165	
Lys	Trp	Lys	Gly	Pro	Gln	Gly	Gln	Asp	Leu	Ser	Thr	Asp	Ser	Arg	
			170			175								180	
Thr	Asn	Arg	Asp	Met	His	Gly	Leu	Phe	Asp	Val	Glu	Ile	Ser	Leu	
			185			190								195	
Thr	Val	Gln	Glu	Asn	Ala	Gly	Ser	Ile	Ser	Cys	Ser	Met	Arg	His	
			200			205								210	
Ala	His	Leu	Ser	Arg	Glu	Val	Glu	Ser	Arg	Val	Gln	Ile	Gly	Asp	
			215			220								225	
Thr	Phe	Phe	Glu	Pro	Ile	Ser	Trp	His	Leu	Ala	Thr	Lys	Val	Leu	
			230			235								240	
Gly	Ile	Leu	Cys	Cys	Gly	Leu	Phe	Phe	Gly	Ile	Val	Gly	Leu	Lys	
			245			250								255	
Ile	Phe	Phe	Ser	Lys	Phe	Gln	Trp	Lys	Ile	Gln	Ala	Glu	Leu	Asp	
			260			265								270	
Trp	Arg	Arg	Lys	His	Gly	Gln	Ala	Glu	Leu	Arg	Asp	Ala	Arg	Lys	
			275			280								285	
His	Ala	Val	Glu	Val	Thr	Leu	Asp	Pro	Glu	Thr	Ala	His	Pro	Lys	

	290	295	300
Leu Cys Val Ser Asp Leu Lys Thr Val Thr His Arg Lys Ala Pro			
305	310	315	
Gln Glu Val Pro His Ser Glu Lys Arg Phe Thr Arg Lys Ser Val			
320	325	330	
Val Ala Ser Gln Ser Phe Gln Ala Gly Lys His Tyr Trp Glu Val			
335	340	345	
Asp Gly Gly His Asn Lys Arg Trp Arg Val Gly Val Cys Arg Asp			
350	355	360	
Asp Val Asp Arg Arg Lys Glu Tyr Val Thr Leu Ser Pro Asp His			
365	370	375	
Gly Tyr Trp Val Leu Arg Leu Asn Gly Glu His Leu Tyr Phe Thr			
380	385	390	
Leu Asn Pro Arg Phe Ile Ser Val Phe Pro Arg Thr Pro Pro Thr			
395	400	405	
Lys Ile Gly Val Phe Leu Asp Tyr Glu Cys Gly Thr Ile Ser Phe			
410	415	420	
Phe Asn Ile Asn Asp Gln Ser Leu Ile Tyr Thr Leu Thr Cys Arg			
425	430	435	
Phe Glu Gly Leu Leu Arg Pro Tyr Ile Glu Tyr Pro Ser Tyr Asn			
440	445	450	
Glu Gln Asn Gly Thr Pro Ile Val Ile Cys Pro Val Thr Gln Glu			
455	460	465	
Ser Glu Lys Glu Ala Ser Trp Gln Arg Ala Ser Ala Ile Pro Glu			
470	475	480	
Thr Ser Asn Ser Glu Ser Ser Gln Ala Thr Thr Pro Phe Leu			
485	490	495	
Pro Arg Gly Glu Met			
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<210> 149
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 149
gcgtggtcca cctctacagg gacg 24

<210> 150
<211> 23

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 150
ggaactgacc cagtgtgac acc 23

<210> 151
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 151
gcagatgcc a c a g t a t c a a g g c a g g a c a a a a c t g g t g a a g g a t t c 45

<210> 152
<211> 2294
<212> DNA
<213> Homo sapiens

<400> 152
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g g t c g g a t t g c a a c g a g g a g a a g a t g a c t g a c c a a c c g a c t g g c a t g 100
a a t g a a t g g c g g a g c g c c a t g a g g a g c c t g c c g a g c c t g g g c g 150
g c c t c g c c t g t g t g c t g c g c c c g c c g c c g t g c c t c a g g c c 200
g c c t c g g c g g g a a t g t c a c c g g t g g c g g c g g g c c g c g g t g g a 250
c g c g t c g c c g g c c c c g g t g c g g g c g a g c c a c c t t c c c t a 300
g g g c g a c g g c c t c c c a c g g c c a g g c c c g g c c c c g c g c c 350
a c c g t c c a c c g c c t g c g a c t t c t c a c c t c a c c t c a c c t c a c c 400
c a c c c t c t t t g g g c g a c t g c t g g a c c c t c t c a c c t c a c c t c a c c 450
c g c t c g g c c c t c g c c g a c c a c c t c c g g c g g a a c g c a c t t c g a c c 500
a c c t c t c a g g c g c c a c c c g c g c c g a c c a c c t t t c a c c t c a c c t c a c c 550
t g g c c c g g c g g c c g a c c a c c a c c t c a c c t c a c c t c a c c t c a c c 600
c t c c c c g g a c c c c c c g a t c t c c c c a c c g a c g c a a a c g c a g c g t c 650
c t c c c c a c c c a c c t g c c a c c c g a g g c c c c c t c t c g c c t c c a g a g t a 700
t g t a t g t a a c t g c t c t g t g g t t g g a a g c c t g a a t g t g a a t c g c t g c a a c c 750
a g a c c a c a g g g c a g t g t g a g t g t c g g c c a g g t t a t c a g g g g c t t c a c t g t 800

gaaacctgca aagagggctt ttacctaaat tacacttctg ggctctgtca 850
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aagcaacaga gggtggaaact gaagtttatt ttatttttagc aaggaaaaaa 950
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agagggagac tctgtcttaa aaaaaaaaaa aaaaaaaaaa aaaa 2294

<210> 153
<211> 258
<212> PRT
<213> Homo sapiens

<400> 153

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						20			25				30	
Val	Thr	Gly	Gly	Gly	Gly	Ala	Ala	Gly	Gln	Val	Asp	Ala	Ser	Pro
		35						40				45		
Gly	Pro	Gly	Leu	Arg	Gly	Glu	Pro	Ser	His	Pro	Phe	Pro	Arg	Ala
	50					55			55			60		
Thr	Ala	Pro	Thr	Ala	Gln	Ala	Pro	Arg	Thr	Gly	Pro	Pro	Arg	Ala
	65						70				75			
Thr	Val	His	Arg	Pro	Leu	Ala	Ala	Thr	Ser	Pro	Ala	Gln	Ser	Pro
	80							85			90			
Glu	Thr	Thr	Pro	Leu	Trp	Ala	Thr	Ala	Gly	Pro	Ser	Ser	Thr	Thr
	95							100			105			
Phe	Gln	Ala	Pro	Leu	Gly	Pro	Ser	Pro	Thr	Thr	Pro	Pro	Ala	Ala
	110						115			115		120		
Glu	Arg	Thr	Ser	Thr	Thr	Ser	Gln	Ala	Pro	Thr	Arg	Pro	Ala	Pro
	125						130			130		135		
Thr	Thr	Leu	Ser	Thr	Thr	Thr	Gly	Pro	Ala	Pro	Thr	Thr	Pro	Val
	140						145			145		150		
Ala	Thr	Thr	Val	Pro	Ala	Pro	Thr	Thr	Pro	Arg	Thr	Pro	Thr	Pro
	155						160			160		165		
Asp	Leu	Pro	Ser	Ser	Ser	Asn	Ser	Ser	Val	Leu	Pro	Thr	Pro	Pro
	170						175			175		180		
Ala	Thr	Glu	Ala	Pro	Ser	Ser	Pro	Pro	Pro	Glu	Tyr	Val	Cys	Asn
	185						190			190		195		
Cys	Ser	Val	Val	Gly	Ser	Leu	Asn	Val	Asn	Arg	Cys	Asn	Gln	Thr
	200							205			205		210	
Thr	Gly	Gln	Cys	Glu	Cys	Arg	Pro	Gly	Tyr	Gln	Gly	Leu	His	Cys
	215						220			220		225		
Glu	Thr	Cys	Lys	Glu	Gly	Phe	Tyr	Leu	Asn	Tyr	Thr	Ser	Gly	Leu
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Cys Gln Pro Cys Asp Cys Ser Pro His Gly Ala Leu Ser Ile Pro
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Cys Asn Arg

<210> 154
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 154
aactgctctg tggttggaag cctg 24

<210> 155
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 155
cagtcacatg gctgacagac ccac 24

<210> 156
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 156
aggttatcag gggcttcaact gtgaaacctg caaagagg 38

<210> 157
<211> 689
<212> DNA
<213> Homo sapiens

<400> 157
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ccggggaaaag ggcttgcca tggagaagga catgaagaac gtcgtgggg 200
tggtggtgac cctcaactcca gaaaacaacc tgcggacgct gtcctctcag 250
cacgggctgg gagggtgtga ccagagtgtc atggacctga taaagcgaaa 300

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agccagccag gaggccatgg ggctttcac caagtggagc aggagcctgg 500
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gggcccagca ccagtcaga ataaagcgat tccacagca 689

<210> 158

<211> 163

<212> PRT

<213> Homo sapiens

<400> 158

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Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys
35 40 45

Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val
50 55 60

Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln
65 70 75

His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys
80 85 90

Arg Asn Ser Gly Trp Val Phe Glu Asn Pro Ser Ile Gly Val Leu
95 100 105

Glu Leu Trp Val Leu Ala Thr Asn Phe Arg Asp Tyr Ala Ile Ile
110 115 120

Phe Thr Gln Leu Glu Phe Gly Asp Glu Pro Phe Asn Thr Val Glu
125 130 135

Leu Tyr Ser Leu Thr Glu Thr Ala Ser Gln Glu Ala Met Gly Leu
140 145 150

Phe Thr Lys Trp Ser Arg Ser Leu Gly Phe Leu Ser Gln
155 160

<210> 159

<211> 1665
<212> DNA
<213> Homo sapiens

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gtaaaactgct gacgatgcag agttccgtga cggtgcagga aggccctgtgt 150
gtccatgtgc cctgctccctt ctccctacccc tcgcatggct ggatttaccc 200
tggcccagta gttcatggct actgggtcccg ggaaggggcc aatacagacc 250
aggatgctcc agtggccaca aacaacccag ctcggcagt gtgggaggag 300
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cctgagcatc agagatgcca gaagaagtga tgcggggaga tacttcttc 400
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ccagcgtgac cacgaacaag accgtccatc tcaacgtgtc ctacccgcct 750
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caccgagatc tcggagatca agatccacag atgagaaact gcagagactc 1450
accctgattg agggatcaca gcccctccag gcaagggaga agtcagaggc 1500
tgattcttgt agaattaaca gccctcaacg tgatgagcta tgataacact 1550
atgaattatg tgcagagtga aaagcacaca ggcttagag tcaaagtatc 1600
tcaaacctga atccacactg tgccctccct tttttttt taactaaaag 1650
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<210> 160

<211> 463

<212> PRT

<213> Homo sapiens

<400> 160

Met Leu Leu Leu Leu Pro Leu Leu Trp Gly Arg Glu Arg Ala
1 5 10 15

Glu Gly Gln Thr Ser Lys Leu Leu Thr Met Gln Ser Ser Val Thr
20 25 30

Val Gln Glu Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr
35 40 45

Pro Ser His Gly Trp Ile Tyr Pro Gly Pro Val Val His Gly Tyr
50 55 60

Trp Phe Arg Glu Gly Ala Asn Thr Asp Gln Asp Ala Pro Val Ala
65 70 75

Thr Asn Asn Pro Ala Arg Ala Val Trp Glu Glu Thr Arg Asp Arg
80 85 90

Phe His Leu Leu Gly Asp Pro His Thr Lys Asn Cys Thr Leu Ser
95 100 105

Ile Arg Asp Ala Arg Arg Ser Asp Ala Gly Arg Tyr Phe Phe Arg
110 115 120

Met Glu Lys Gly Ser Ile Lys Trp Asn Tyr Lys His His Arg Leu
125 130 135

Ser Val Asn Val Thr Ala Leu Thr His Arg Pro Asn Ile Leu Ile
140 145 150

Pro Gly Thr Leu Glu Ser Gly Cys Pro Gln Asn Leu Thr Cys Ser
155 160 165

Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met Ile Ser Trp
170 175 180

Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr Arg Ser
185 190 195

Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr Ser
200 205 210

Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn
215 220 225

Lys Thr Val His Leu Asn Val Ser Tyr Pro Pro Gln Asn Leu Thr
230 235 240

Met Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly
245 250 255

Asn Gly Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu
260 265 270

Val Cys Ala Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu
275 280 285

Ser Leu Ser Trp Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser
290 295 300

Asn Pro Gly Val Leu Glu Leu Pro Trp Val His Leu Arg Asp Ala
305 310 315

Ala Glu Phe Thr Cys Arg Ala Gln Asn Pro Leu Gly Ser Gln Gln
320 325 330

Val Tyr Leu Asn Val Ser Leu Gln Ser Lys Ala Thr Ser Gly Val
335 340 345

Thr Gln Gly Val Val Gly Gly Ala Gly Ala Thr Ala Leu Val Phe
350 355 360

Leu Ser Phe Cys Val Ile Phe Val Val Arg Ser Cys Arg Lys
365 370 375

Lys Ser Ala Arg Pro Ala Ala Gly Val Gly Asp Thr Gly Ile Glu
380 385 390

Asp Ala Asn Ala Val Arg Gly Ser Ala Ser Gln Gly Pro Leu Thr
395 400 405

Glu Pro Trp Ala Glu Asp Ser Pro Pro Asp Gln Pro Pro Pro Ala
410 415 420

Ser Ala Arg Ser Ser Val Gly Glu Gly Glu Leu Gln Tyr Ala Ser
425 430 435

Leu Ser Phe Gln Met Val Lys Pro Trp Asp Ser Arg Gly Gln Glu
440 445 450

Ala Thr Asp Thr Glu Tyr Ser Glu Ile Lys Ile His Arg
455 460

<210> 161
<211> 739
<212> DNA
<213> Homo sapiens

<400> 161
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accctgttcc tgggtgtcac gctcggcctg gccgctgccc tgtccttcac 100
cctggaggag gaggatatca cagggacctg gtacgtgaag gccatggtgg 150
tcgataagga ctttccggag gacaggaggc ccaggaaggt gtccccagtg 200
aaggtgacag ccctggcg 500
tgggaagttg gaagccacgt tcaccttcac 250
gagggaggat cggtgcattcc agaagaaaat cctgatgcgg aagacggagg 300
agcctggcaa atacagcgcc tatggggca ggaagctcat gtacctgcag 350
gagctgccc 500
ggagggacca ctacatctt tactgcaaag accagcacca 400
tggggcctg ctccacatgg gaaagcttgc 500
ggtaggaat tctgatacc 450
accgggaggc cctggaagaa tttaagaaaat tggtgcagcg caagggactc 500
tcggaggagg acatttcac gcccctgcag acggaaagct gcgttcccga 550
acactaggca gccccgggt ctgcaccc 500
tccaccacc 600
acacagagcc cgaccaccc 500
ggacctaccc tccagccatg accctccct 650
gctcccaccc acctgactcc aaataaagtc cttttcccc aaaaaaaaaa 700
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162
<211> 170
<212> PRT
<213> Homo sapiens

<400> 162
Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala
1 5 10 15
Leu Ser Phe Thr Leu Glu Glu Asp Ile Thr Gly Thr Trp Tyr
20 25 30
Val Lys Ala Met Val Val Asp Lys Asp Phe Pro Glu Asp Arg Arg
35 40 45
Pro Arg Lys Val Ser Pro Val Lys Val Thr Ala Leu Gly Gly
50 55 60
Lys Leu Glu Ala Thr Phe Thr Phe Met Arg Glu Asp Arg Cys Ile
65 70 75

Gln Lys Lys Ile Leu Met Arg Lys Thr Glu Glu Pro Gly Lys Tyr
80 85 90

Ser Ala Tyr Gly Gly Arg Lys Leu Met Tyr Leu Gln Glu Leu Pro
95 100 105

Arg Arg Asp His Tyr Ile Phe Tyr Cys Lys Asp Gln His His Gly
110 115 120

Gly Leu Leu His Met Gly Lys Leu Val Gly Arg Asn Ser Asp Thr
125 130 135

Asn Arg Glu Ala Leu Glu Glu Phe Lys Lys Leu Val Gln Arg Lys
140 145 150

Gly Leu Ser Glu Glu Asp Ile Phe Thr Pro Leu Gln Thr Gly Ser
155 160 165

Cys Val Pro Glu His
170

<210> 163

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 163

ggagatgaag accctgttcc tg 22

<210> 164

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 164

ggagatgaag accctgttcc tgggtg 26

<210> 165

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 165

gtcctccgga aagtccatat c 21

<210> 166

<211> 25

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 166
gcctagtgtt cggaaacgca gcttc 25

<210> 167
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 167
cagggacctg gtacgtgaag gccatggtgg tcgataagga ctttccggag 50

<210> 168
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 168
ctgtccttca ccctggagga ggaggatatac acagggacct ggtac 45

<210> 169
<211> 1204
<212> DNA
<213> Homo sapiens

<400> 169
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cagaggtctc acagcagcca aggaacctgg ggcccgtcc tccccctcc 100
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggtt 150
gtagggggag agaccaggat catcaagggg ttcgagtgca agcctcactc 200
ccagccctgg caggcagccc tggcgagaa gacgcggcta ctctgtgggg 250
cgacgctcat cgccccaga tggctcctga cagcagcccc ctgcctcaag 300
ccccgctaca tagttcacct ggggcagcac aacctccaga aggaggagg 350
ctgtgagcag acccggacag ccactgagtc cttccccac cccggcttca 400
acaacagcct ccccaacaaa gaccaccgca atgacatcat gctggtaag 450
atggcatcgc cagtctccat cacctgggct gtgcgacccc tcaccctctc 500

ctcacgcgtg gtcactgctg gcaccagctg ctcatttcc ggctggggca 550
gcacgtccag cccccagtta cgccctgcctc acaccttgcg atgcgccaac 600
atcaccatca ttgagcacca gaagtgtgag aacgcctacc ccggcaacat 650
cacagacacc atggtgtgtg ccagcgtgca ggaagggggc aaggactcct 700
gccagggtga ctccggggc cctctggtct gtaaccagtc tcttcaaggc 750
attatctcct gggccagga tccgtgtgcg atcaccgaa agcctggtgt 800
ctacacgaaa gtctgcaa atgtggactg gatccaggag acgatgaaga 850
acaatttagac tggacccacc caccacagcc catcaccctc catttccact 900
tggtgtttgg ttccctgttca ctctgttaat aagaaaccct aagccaagac 950
cctctacgaa cattcttgg gcctcctgga ctacaggaga tgctgtcact 1000
taataatcaa cctggggttc gaaatcagtg agacctggat tcaaattctg 1050
ccttgaataa ttgtgactct gggaatgaca acacctggtt tgttctgt 1100
tgtatccccca gccccaaaga cagctcctgg ccatatatca aggttcaat 1150
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aaaa 1204

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<210> 170
<211> 250
<212> PRT
<213> Homo sapiens

<400> 170
Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu
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Val Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro
   20          25          30

His Ser Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu
   35          40          45

Leu Cys Gly Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala
   50          55          60

Ala His Cys Leu Lys Pro Arg Tyr Ile Val His Leu Gly Gln His
   65          70          75

Asn Leu Gln Lys Glu Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr
   80          85          90

Glu Ser Phe Pro His Pro Gly Phe Asn Asn Ser Leu Pro Asn Lys
   95         100         105

```

Asp His Arg Asn Asp Ile Met Leu Val Lys Met Ala Ser Pro Val
110 115 120

Ser Ile Thr Trp Ala Val Arg Pro Leu Thr Leu Ser Ser Arg Cys
125 130 135

Val Thr Ala Gly Thr Ser Cys Leu Ile Ser Gly Trp Gly Ser Thr
140 145 150

Ser Ser Pro Gln Leu Arg Leu Pro His Thr Leu Arg Cys Ala Asn
155 160 165

Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn Ala Tyr Pro Gly
170 175 180

Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln Glu Gly Gly
185 190 195

Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Asn
200 205 210

Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys Ala
215 220 225

Ile Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr Val
230 235 240

Asp Trp Ile Gln Glu Thr Met Lys Asn Asn
245 250

<210> 171

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 171

ggctgcggga ctggaagtca tcggg 25

<210> 172

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 172

ctccaggcca tgaggattct gcag 24

<210> 173

<211> 18

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 173
cctctggtct gtaaccag 18

<210> 174
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 174
tctgtgatgt tgccgggta ggcg 24

<210> 175
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 175
cgttagaca ccaggcttc gggtg 25

<210> 176
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 176
cccttgatga tcctggtc 18

<210> 177
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 177
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggtt 50

<210> 178
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 178
gagagaccag gatcatcaag gggttcgagt gcaaggctca ctc 43

<210> 179
<211> 907
<212> DNA
<213> Homo sapiens

<400> 179
gagcagtgtt ctgctggagc cgatgc当地 aaccatgc当地 ttcttattca 50
gattcattgt tttctttat ctgtgggccc ttttactgc tcagagacaa 100
aagaaaagagg agagcaccga agaagtgaaa atagaagttt tgc当地gtcc 150
agaaaaactgc tctaagacaa gcaagaaggg agacctacta aatgccatt 200
atgacggcta cctggctaaa gacggctcg aattctactg cagccggaca 250
caaaaatgaag gccaccccaa atggttgtt ctgggtgtt ggcaagtc当地 300
aaaaggccta gacattgcta tgacagatat gtgc当地tggaa gaaaagcgaa 350
aagtagttat acccccttca tttgcatacg gaaaggaagg ctatgc当地aa 400
ggcaagattc caccggatgc tacattgatt tttgagattt aactttatgc 450
tgtgaccaaa ggaccacgga gcattgagac atttaaacaa atagacatgg 500
acaatgacag gcagctctct aaagccgaga taaacctcta cttgcaaaagg 550
gaatttgaaa aagatgagaa gccacgtgac aagtcatatc aggatgc当地 600
tttagaagat attttaaga agaatgacca tgatggtgat ggcttc当地ttt 650
ctcccaagga atacaatgta taccaacacg atgaactata gcatatttgc 700
atttctactt tttttttta gctatttact gtactttatg tataaaaacaa 750
agtcaactttt ctccaagttt tatttgctat tttccctta tgagaagata 800
tttgatctc cccaatacat tgattttggat ataataatg tgaggctgtt 850
ttgcaaactt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900
aaaaaaaa 907

<210> 180
<211> 222
<212> PRT
<213> Homo sapiens

<400> 180
Met Pro Lys Thr Met His Phe Leu Phe Arg Phe Ile Val Phe Phe
1 5 10 15

Tyr Leu Trp Gly Leu Phe Thr Ala Gln Arg Gln Lys Lys Glu Glu
20 25 30

Ser Thr Glu Glu Val Lys Ile Glu Val Leu His Arg Pro Glu Asn
35 40 45

Cys Ser Lys Thr Ser Lys Lys Gly Asp Leu Leu Asn Ala His Tyr
50 55 60

Asp Gly Tyr Leu Ala Lys Asp Gly Ser Lys Phe Tyr Cys Ser Arg
65 70 75

Thr Gln Asn Glu Gly His Pro Lys Trp Phe Val Leu Gly Val Gly
80 85 90

Gln Val Ile Lys Gly Leu Asp Ile Ala Met Thr Asp Met Cys Pro
95 100 105

Gly Glu Lys Arg Lys Val Val Ile Pro Pro Ser Phe Ala Tyr Gly
110 115 120

Lys Glu Gly Tyr Ala Glu Gly Lys Ile Pro Pro Asp Ala Thr Leu
125 130 135

Ile Phe Glu Ile Glu Leu Tyr Ala Val Thr Lys Gly Pro Arg Ser
140 145 150

Ile Glu Thr Phe Lys Gln Ile Asp Met Asp Asn Asp Arg Gln Leu
155 160 165

Ser Lys Ala Glu Ile Asn Leu Tyr Leu Gln Arg Glu Phe Glu Lys
170 175 180

Asp Glu Lys Pro Arg Asp Lys Ser Tyr Gln Asp Ala Val Leu Glu
185 190 195

Asp Ile Phe Lys Lys Asn Asp His Asp Gly Asp Gly Phe Ile Ser
200 205 210

Pro Lys Glu Tyr Asn Val Tyr Gln His Asp Glu Leu
215 220

<210> 181

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 181

gtgttctgct ggagccgatg cc 22

<210> 182

<211> 18

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 182
gacatggaca atgacagg 18

<210> 183
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 183
ccttcagga tgttaggag 18

<210> 184
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 184
gatgtctgcc accccaag 18

<210> 185
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 185
gcatcctgat atgacttgac acgtggc 27

<210> 186
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 186
tacaagaggg aagaggagg 24

<210> 187
<211> 52
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 187

gcccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50

cc 52

<210> 188

<211> 573

<212> DNA

<213> Homo sapiens

<400> 188

cagaaatgca gggaccattg cttcttccag gcctctgctt tctgctgagc 50

ctctttggag ctgtgactca gaaaacccaaa acttcctgtg ctaagtgc 100

cccaaatgct tcctgtgtca ataacactca ctgcacctgc aaccatggat 150

ataacttctgg atctggcag aaactattca cattccccctt ggagacatgt 200

aacgccaggc atggcggctc gcgcctgtaa tcccaaggatct ttgggaagcc 250

aaggcaggc gatcacctga ggtcaggagt ttgagaccag cctggccaac 300

atagtgaaac cccgtgtcta ctaaaaatac aaaaatcagc cgggcgttgt 350

ggtgcatgcc tgcaatcccc gttactcggg aggctgaggc aggagaatcg 400

cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450

ctccagcatg gatgacagag caagactccg tctaaaaag aaaagatagt 500

ttcttgtttc atttcgcgac tgccctctca gtgttcctg ggatccccctc 550

ccaaataaag tacttatatt ctc 573

<210> 189

<211> 74

<212> PRT

<213> Homo sapiens

<400> 189

Met Gln Gly Pro Leu Leu Leu Pro Gly Leu Cys Phe Leu Leu Ser
1 5 10 15

Leu Phe Gly Ala Val Thr Gln Lys Thr Lys Thr Ser Cys Ala Lys
20 25 30

Cys Pro Pro Asn Ala Ser Cys Val Asn Asn Thr His Cys Thr Cys
35 40 45

Asn His Gly Tyr Thr Ser Gly Ser Gly Gln Lys Leu Phe Thr Phe
50 55 60

Pro Leu Glu Thr Cys Asn Ala Arg His Gly Gly Ser Arg Leu
65 70

<210> 190
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 190
agggaccatt gcttcttcca ggcc 24

<210> 191
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 191
cgttacatgt ctccaagggg aatg 24

<210> 192
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 192
cctgtgctaa gtgcccccca aatgcttcct gtgtcaataa cactcactgc 50

<210> 193
<211> 1091
<212> DNA
<213> Homo sapiens

<400> 193
caagcaggc atccccttgg tgaccttcaa agagaagcag agagggcaga 50
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gactttggaa gtgaccaccatggggctca gcattttt gtcctgtgt 150
gttcttggc tcagccaggc agccacaccg aagatttca atggcactga 200
gtgtggcgt aactcacagc cgtggcaggt ggggctgttt gagggcacca 250
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gctcactgca gcggcagcag gtactgggtg cgcctgggg aacacagcct 350
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cccatcccggtt cttttttttt cttttttttt 450

ctgctgcggc tgcgcctgcc cgtccgcgta accagcagcg ttcaaccct 500
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gctggggcat caccaaccac ccacggaacc cattcccgga tctgctccag 600
tgccctcaacc tctccatcgt ctccccatgcc acctgccatg gtgtgtatcc 650
cgggagaatc acgagcaaca tggtgtgtgc aggccggcgtc ccggggcagg 700
atgcctgcca gggtgattct gggggcccccc tggtgtgtgg gggagtcctt 750
caaggtctgg tggctgggg gtctgtgggg ccctgtggac aagatggcat 800
ccctggagtc tacacctata tttgcaagta tgtggactgg atccggatga 850
tcatgagaa caactgacct gttccctcca cctccacccc cacccttaa 900
cttgggtacc cctctggccc tcagagcacc aatatctcct ccatcacttc 950
ccctagctcc actcttggttg gcctggAAC ttcttggAAC tttaactcct 1000
gccagccctt ctaagaccca cgagcggggt gagagaagtg tgcaatagtc 1050
tggaaaaat ataaatgaag gaggggcaaa aaaaaaaaaa a 1091

<210> 194
<211> 248
<212> PRT
<213> Homo sapiens

<400> 194
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1 5 10 15
Gln Ala Ala Thr Pro Lys Ile Phe Asn Gly Thr Glu Cys Gly Arg
20 25 30
Asn Ser Gln Pro Trp Gln Val Gly Leu Phe Glu Gly Thr Ser Leu
35 40 45
Arg Cys Gly Gly Val Leu Ile Asp His Arg Trp Val Leu Thr Ala
50 55 60
Ala His Cys Ser Gly Ser Arg Tyr Trp Val Arg Leu Gly Glu His
65 70 75
Ser Leu Ser Gln Leu Asp Trp Thr Glu Gln Ile Arg His Ser Gly
80 85 90
Phe Ser Val Thr His Pro Gly Tyr Leu Gly Ala Ser Thr Ser His
95 100 105
Glu His Asp Leu Arg Leu Leu Arg Leu Arg Leu Pro Val Arg Val
110 115 120

Thr Ser Ser Val Gln Pro Leu Pro Leu Pro Asn Asp Cys Ala Thr
125 130 135
Ala Gly Thr Glu Cys His Val Ser Gly Trp Gly Ile Thr Asn His
140 145 150
Pro Arg Asn Pro Phe Pro Asp Leu Leu Gln Cys Leu Asn Leu Ser
155 160 165
Ile Val Ser His Ala Thr Cys His Gly Val Tyr Pro Gly Arg Ile
170 175 180
Thr Ser Asn Met Val Cys Ala Gly Gly Val Pro Gly Gln Asp Ala
185 190 195
Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly Val Leu
200 205 210
Gln Gly Leu Val Ser Trp Gly Ser Val Gly Pro Cys Gly Gln Asp
215 220 225
Gly Ile Pro Gly Val Tyr Thr Tyr Ile Cys Lys Tyr Val Asp Trp
230 235 240
Ile Arg Met Ile Met Arg Asn Asn
245

<210> 195
<211> 1485
<212> DNA
<213> Homo sapiens

<400> 195
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ctcgccctc gccgcgtccg cgaagcctgg agccggcgaa agcccccgcgc 100
tcgccccatgtc gggcgagctc agcaacaggt tccaaggagg gaaggcggtc 150
ggcttgctca aagccccggca ggagaggagg ctggccgaga tcaaccggga 200
gtttctgtgt gaccagaagt acagtgtatga agagaacattt ccagaaaagc 250
tcacagcctt caaagagaag tacatggagt ttgacactgaa caatgaaggc 300
gagattgacc tggatgtcttt aaagaggatg atggagaagc ttgggtgtccc 350
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tcagtgacac tatatcctac cgagactttt tgaacatgtat gctggggaaa 450
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ctcccgatct tgctgccctt cttgacacac tgtgatctct ctctctctca 650
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cttccagcct gtgttcccct cacttggagg aaccagcact ctccatcctt 900
tcagaaagtc tccaagccaa gttcaggctc actgacctgg ctctgacgag 950
gaccccaggg cactctgaga agaccttgga gtagggacaa ggctgcaggg 1000
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accaggaca cagccactcg gggcccccgt gcccagctg atccccactc 1100
attccacacc tcttctcatc ctcagtatg tgaaggtggg aaggaaagga 1150
gcttggcatt gggagccctt caagaaggtt ccagaaggaa ccctccagtc 1200
ctgctctctg gccacacctg tgcaggcagc tgagaggcag cgtgcagccc 1250
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gatactgagg ggaccaggat gggagaatga ggagtaaat gtcacggca 1400
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tgaccccaat ctgcttggaaa aaaaaaaaaa aaaaaa 1485

<210> 196
<211> 150
<212> PRT
<213> Homo' sapiens

<400> 196
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20 25 30
Arg Glu Phe Leu Cys Asp Gln Lys Tyr Ser Asp Glu Glu Asn Leu
35 40 45
Pro Glu Lys Leu Thr Ala Phe Lys Glu Lys Tyr Met Glu Phe Asp
50 55 60
Leu Asn Asn Glu Gly Glu Ile Asp Leu Met Ser Leu Lys Arg Met
65 70 75

Met Glu Lys Leu Gly Val Pro Lys Thr His Leu Glu Met Lys Lys
80 85 90

Met Ile Ser Glu Val Thr Gly Gly Val Ser Asp Thr Ile Ser Tyr
95 100 105

Arg Asp Phe Val Asn Met Met Leu Gly Lys Arg Ser Ala Val Leu
110 115 120

Lys Leu Val Met Met Phe Glu Gly Lys Ala Asn Glu Ser Ser Pro
125 130 135

Lys Pro Val Gly Pro Pro Pro Glu Arg Asp Ile Ala Ser Leu Pro
140 145 150

<210> 197

<211> 4842

<212> DNA

<213> Homo sapiens

<400> 197

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ggggtcggcg ccgcgtgcg cgccgcctg gcgctggcct tggcgctggc 150

gagcgtcctg agtgggcctc cagccgtcgc ctgccccacc aagtgtacct 200

gctccgctgc cagcgtggac tgccacgggc tggcctccg cgccgttcct 250

cggggcatcc cccgcaacgc tgagcgcctt gacctggaca gaaataatat 300

caccaggatc accaagatgg acttcgttg gctcaagaac ctccgagtct 350

tgcattctgga agacaaccag gtcagcgtca tcgagagagg cgccttccag 400

gacctgaagc agctagagcg actgcgcctg aacaagaata agctgcaagt 450

ccttccagaa ttgctttcc agagcacgcc gaagctcacc agactagatt 500

tgagtgaaaa ccagatccag gggatcccgaa ggaaggcggtt ccgcggcatc 550

accgatgtga agaacctgca actggacaac aaccacatca gctgcattga 600

agatggagcc ttccgagcgc tgcgcgattt ggagatcctt accctcaaca 650

acaacaacat cagtcgcattc ctggtcacca gcttcaacca catgccgaag 700

atccgaactc tgccctcca ctccaaccac ctctactgcg actgccacct 750

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cagaagaagg agtacgtgtg cccagccccc cactcggagc ccccatcctg 900

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<210> 198
<211> 1523
<212> PRT
<213> Homo sapiens

<400> 198
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Leu Ala Leu Ala Leu Ala Leu Ala Ser Val Leu Ser Gly Pro Pro
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Ala Val Ala Cys Pro Thr Lys Cys Thr Cys Ser Ala Ala Ser Val

	35	40	45
Asp Cys His Gly Leu Gly Leu Arg Ala Val Pro Arg Gly Ile Pro			
50	55	60	
Arg Asn Ala Glu Arg Leu Asp Leu Asp Arg Asn Asn Ile Thr Arg			
65	70	75	
Ile Thr Lys Met Asp Phe Ala Gly Leu Lys Asn Leu Arg Val Leu			
80	85	90	
His Leu Glu Asp Asn Gln Val Ser Val Ile Glu Arg Gly Ala Phe			
95	100	105	
Gln Asp Leu Lys Gln Leu Glu Arg Leu Arg Leu Asn Lys Asn Lys			
110	115	120	
Leu Gln Val Leu Pro Glu Leu Leu Phe Gln Ser Thr Pro Lys Leu			
125	130	135	
Thr Arg Leu Asp Leu Ser Glu Asn Gln Ile Gln Gly Ile Pro Arg			
140	145	150	
Lys Ala Phe Arg Gly Ile Thr Asp Val Lys Asn Leu Gln Leu Asp			
155	160	165	
Asn Asn His Ile Ser Cys Ile Glu Asp Gly Ala Phe Arg Ala Leu			
170	175	180	
Arg Asp Leu Glu Ile Leu Thr Leu Asn Asn Asn Ile Ser Arg			
185	190	195	
Ile Leu Val Thr Ser Phe Asn His Met Pro Lys Ile Arg Thr Leu			
200	205	210	
Arg Leu His Ser Asn His Leu Tyr Cys Asp Cys His Leu Ala Trp			
215	220	225	
Leu Ser Asp Trp Leu Arg Gln Arg Arg Thr Val Gly Gln Phe Thr			
230	235	240	
Leu Cys Met Ala Pro Val His Leu Arg Gly Phe Asn Val Ala Asp			
245	250	255	
Val Gln Lys Lys Glu Tyr Val Cys Pro Ala Pro His Ser Glu Pro			
260	265	270	
Pro Ser Cys Asn Ala Asn Ser Ile Ser Cys Pro Ser Pro Cys Thr			
275	280	285	
Cys Ser Asn Asn Ile Val Asp Cys Arg Gly Lys Gly Leu Met Glu			
290	295	300	
Ile Pro Ala Asn Leu Pro Glu Gly Ile Val Glu Ile Arg Leu Glu			
305	310	315	
Gln Asn Ser Ile Lys Ala Ile Pro Ala Gly Ala Phe Thr Gln Tyr			

320 325 330
Lys Lys Leu Lys Arg Ile Asp Ile Ser Lys Asn Gln Ile Ser Asp
335 340 345
Ile Ala Pro Asp Ala Phe Gln Gly Leu Lys Ser Leu Thr Ser Leu
350 355 360
Val Leu Tyr Gly Asn Lys Ile Thr Glu Ile Ala Lys Gly Leu Phe
365 370 375
Asp Gly Leu Val Ser Leu Gln Leu Leu Leu Leu Asn Ala Asn Lys
380 385 390
Ile Asn Cys Leu Arg Val Asn Thr Phe Gln Asp Leu Gln Asn Leu
395 400 405
Asn Leu Leu Ser Leu Tyr Asp Asn Lys Leu Gln Thr Ile Ser Lys
410 415 420
Gly Leu Phe Ala Pro Leu Gln Ser Ile Gln Thr Leu His Leu Ala
425 430 435
Gln Asn Pro Phe Val Cys Asp Cys His Leu Lys Trp Leu Ala Asp
440 445 450
Tyr Leu Gln Asp Asn Pro Ile Glu Thr Ser Gly Ala Arg Cys Ser
455 460 465
Ser Pro Arg Arg Leu Ala Asn Lys Arg Ile Ser Gln Ile Lys Ser
470 475 480
Lys Lys Phe Arg Cys Ser Gly Ser Glu Asp Tyr Arg Ser Arg Phe
485 490 495
Ser Ser Glu Cys Phe Met Asp Leu Val Cys Pro Glu Lys Cys Arg
500 505 510
Cys Glu Gly Thr Ile Val Asp Cys Ser Asn Gln Lys Leu Val Arg
515 520 525
Ile Pro Ser His Leu Pro Glu Tyr Val Thr Asp Leu Arg Leu Asn
530 535 540
Asp Asn Glu Val Ser Val Leu Glu Ala Thr Gly Ile Phe Lys Lys
545 550 555
Leu Pro Asn Leu Arg Lys Ile Asn Leu Ser Asn Asn Lys Ile Lys
560 565 570
Glu Val Arg Glu Gly Ala Phe Asp Gly Ala Ala Ser Val Gln Glu
575 580 585
Leu Met Leu Thr Gly Asn Gln Leu Glu Thr Val His Gly Arg Val
590 595 600
Phe Arg Gly Leu Ser Gly Leu Lys Thr Leu Met Leu Arg Ser Asn

605 610 615
Leu Ile Ser Cys Val Ser Asn Asp Thr Phe Ala Gly Leu Ser Ser
620 625 630
Val Arg Leu Leu Ser Leu Tyr Asp Asn Arg Ile Thr Thr Ile Thr
635 640 645
Pro Gly Ala Phe Thr Thr Leu Val Ser Leu Ser Thr Ile Asn Leu
650 655 660
Leu Ser Asn Pro Phe Asn Cys Asn Cys His Leu Ala Trp Leu Gly
665 670 675
Lys Trp Leu Arg Lys Arg Arg Ile Val Ser Gly Asn Pro Arg Cys
680 685 690
Gln Lys Pro Phe Phe Leu Lys Glu Ile Pro Ile Gln Asp Val Ala
695 700 705
Ile Gln Asp Phe Thr Cys Asp Gly Asn Glu Glu Ser Ser Cys Gln
710 715 720
Leu Ser Pro Arg Cys Pro Glu Gln Cys Thr Cys Met Glu Thr Val
725 730 735
Val Arg Cys Ser Asn Lys Gly Leu Arg Ala Leu Pro Arg Gly Met
740 745 750
Pro Lys Asp Val Thr Glu Leu Tyr Leu Glu Gly Asn His Leu Thr
755 760 765
Ala Val Pro Arg Glu Leu Ser Ala Leu Arg His Leu Thr Leu Ile
770 775 780
Asp Leu Ser Asn Asn Ser Ile Ser Met Leu Thr Asn Tyr Thr Phe
785 790 795
Ser Asn Met Ser His Leu Ser Thr Leu Ile Leu Ser Tyr Asn Arg
800 805 810
Leu Arg Cys Ile Pro Val His Ala Phe Asn Gly Leu Arg Ser Leu
815 820 825
Arg Val Leu Thr Leu His Gly Asn Asp Ile Ser Ser Val Pro Glu
830 835 840
Gly Ser Phe Asn Asp Leu Thr Ser Leu Ser His Leu Ala Leu Gly
845 850 855
Thr Asn Pro Leu His Cys Asp Cys Ser Leu Arg Trp Leu Ser Glu
860 865 870
Trp Val Lys Ala Gly Tyr Lys Glu Pro Gly Ile Ala Arg Cys Ser
875 880 885
Ser Pro Glu Pro Met Ala Asp Arg Leu Leu Leu Thr Thr Pro Thr

890 895 900
His Arg Phe Gln Cys Lys Gly Pro Val Asp Ile Asn Ile Val Ala
905 910 915
Lys Cys Asn Ala Cys Leu Ser Ser Pro Cys Lys Asn Asn Gly Thr
920 925 930
Cys Thr Gln Asp Pro Val Glu Leu Tyr Arg Cys Ala Cys Pro Tyr
935 940 945
Ser Tyr Lys Gly Lys Asp Cys Thr Val Pro Ile Asn Thr Cys Ile
950 955 960
Gln Asn Pro Cys Gln His Gly Gly Thr Cys His Leu Ser Asp Ser
965 970 975
His Lys Asp Gly Phe Ser Cys Ser Cys Pro Leu Gly Phe Glu Gly
980 985 990
Gln Arg Cys Glu Ile Asn Pro Asp Asp Cys Glu Asp Asn Asp Cys
995 1000 1005
Glu Asn Asn Ala Thr Cys Val Asp Gly Ile Asn Asn Tyr Val Cys
1010 1015 1020
Ile Cys Pro Pro Asn Tyr Thr Gly Glu Leu Cys Asp Glu Val Ile
1025 1030 1035
Asp His Cys Val Pro Glu Leu Asn Leu Cys Gln His Glu Ala Lys
1040 1045 1050
Cys Ile Pro Leu Asp Lys Gly Phe Ser Cys Glu Cys Val Pro Gly
1055 1060 1065
Tyr Ser Gly Lys Leu Cys Glu Thr Asp Asn Asp Asp Cys Val Ala
1070 1075 1080
His Lys Cys Arg His Gly Ala Gln Cys Val Asp Thr Ile Asn Gly
1085 1090 1095
Tyr Thr Cys Thr Cys Pro Gln Gly Phe Ser Gly Pro Phe Cys Glu
1100 1105 1110
His Pro Pro Pro Met Val Leu Leu Gln Thr Ser Pro Cys Asp Gln
1115 1120 1125
Tyr Glu Cys Gln Asn Gly Ala Gln Cys Ile Val Val Gln Gln Glu
1130 1135 1140
Pro Thr Cys Arg Cys Pro Pro Gly Phe Ala Gly Pro Arg Cys Glu
1145 1150 1155
Lys Leu Ile Thr Val Asn Phe Val Gly Lys Asp Ser Tyr Val Glu
1160 1165 1170
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1175 1180 1185
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1250 1255 1260
Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser
1265 1270 1275
Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala
1280 1285 1290
Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys
1295 1300 1305
Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala
1310 1315 1320
Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys
1325 1330 1335
Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser
1340 1345 1350
Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp
1355 1360 1365
Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly
1370 1375 1380
Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu
1385 1390 1395
Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn
1400 1405 1410
Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser
1415 1420 1425
Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly
1430 1435 1440
Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg
1445 1450 1455
Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala

1460 1465 1470

Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln
1475 1480 1485

Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln
1490 1495 1500

Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu
1505 1510 1515

Glu Cys Gly Cys Leu Ala Cys Ser
1520

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<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 199
atggagattc ctgccaactt gccg 24

<210> 200
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 200
ttgttggcat tgaggaggag cagc 24

<210> 201
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 201
gagggcatcg tcgaaatacg cctagaacag aactccatca aagccatccc 50

<210> 202
<211> 753
<212> DNA
<213> Homo sapiens

<400> 202
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gtttcttccg cagactcaac tgagaagtca gcctctgggg caggcaccag 100

gaatctgcct tttcagttct gtctccggca ggcttgagg atgaaggctg 150
cgggcattct gaccctcatt ggctgcctgg tcacaggcgc cgagtccaaa 200.
atctacactc gttgcaaact ggcaaaaata ttctcgaggg ctggcctgga 250.
caattactgg ggcttcagcc ttggaaactg gatctgcattg gcatattatg 300
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gtc 753

<210> 203
<211> 148
<212> PRT
<213> Homo sapiens

<400> 203

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					20				25					30
Phe	Ser	Arg	Ala	Gly	Leu	Asp	Asn	Tyr	Trp	Gly	Phe	Ser	Leu	Gly
					35				40					45
Asn	Trp	Ile	Cys	Met	Ala	Tyr	Tyr	Glu	Ser	Gly	Tyr	Asn	Thr	Thr
					50				55					60
Ala	Pro	Thr	Val	Leu	Asp	Asp	Gly	Ser	Ile	Asp	Tyr	Gly	Ile	Phe
					65				70					75
Gln	Ile	Asn	Ser	Phe	Ala	Trp	Cys	Arg	Arg	Gly	Lys	Leu	Lys	Glu
					80				85					90
Asn	Asn	His	Cys	His	Val	Ala	Cys	Ser	Ala	Leu	Ile	Thr	Asp	Asp
					95				100					105
Leu	Thr	Asp	Ala	Ile	Ile	Cys	Ala	Arg	Lys	Ile	Val	Lys	Glu	Thr
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Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser
140 145

<210> 204

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 204

gcaggcttg aggatgaagg ctgc 24

<210> 205

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 205

ctcattggct gcctggtcac aggc 24

<210> 206

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 206

ccagtcggac aggtctctcc cctc 24

<210> 207

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 207

tcagtgacca aggctgagca ggcg 24

<210> 208

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 208

ctacactcgt tgcaaactgg caaaaatatt ctcgagggct ggcctgg 47

<210> 209

<211> 1648

<212> DNA

<213> Homo sapiens

<400> 209

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ctttttacct tggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200

gcggaagaag atcctatTTT actgtcactt cccagatctg cttctcacca 250

agagagattc ttttcttaaa cgactataca gggccccaat tgactggata 300

gaggaataca ccacaggcat ggcagactgc atcttagtca acagccagtt 350

cacagctgct gttttaagg aaacattcaa gtccctgtct cacatagacc 400

ctgatgtcct ctatccatct ctaaatgtca ccagcttga ctcagttgtt 450

cctgaaaAGC tggatgacct agtccccaaAG gggaaaaAA tcctgctgct 500

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ccctagtaca gctgcgtgga agattgacat cccaaGATTG ggagaggGTT 600

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acattatcag gaattgaaga aaatggtcca acagtccgac cttggccagt 700

atgtgacctt cttgaggtct ttctcagaca aacagaaaaat ctccctcctc 750

cacagctgca cgtgtgtgct ttacacacca agcaatgagc actttggcat 800

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aaactgctgg tataatcaga ttgttttaa gatctccatt aatgtcattt 1100

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<210> 210

<211> 323

<212> PRT

<213> Homo sapiens

<400> 210

Met Pro Leu Leu Lys Leu Val His Gly Ser Pro Leu Val Phe Gly
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Glu Lys Phe Lys Leu Phe Thr Leu Val Ser Ala Cys Ile Pro Val
20 25 30

Phe Arg Leu Ala Arg Arg Lys Lys Ile Leu Phe Tyr Cys His
35 40 45

Phe Pro Asp Leu Leu Thr Lys Arg Asp Ser Phe Leu Lys Arg
50 55 60

Leu Tyr Arg Ala Pro Ile Asp Trp Ile Glu Glu Tyr Thr Thr Gly
65 70 75

Met Ala Asp Cys Ile Leu Val Asn Ser Gln Phe Thr Ala Ala Val
80 85 90

Phe Lys Glu Thr Phe Lys Ser Leu Ser His Ile Asp Pro Asp Val
95 100 105

Leu Tyr Pro Ser Leu Asn Val Thr Ser Phe Asp Ser Val Val Pro
110 115 120

Glu Lys Leu Asp Asp Leu Val Pro Lys Gly Lys Lys Phe Leu Leu
125 130 135

Leu Ser Ile Asn Arg Tyr Glu Arg Lys Lys Asn Leu Thr Leu Ala
140 145 150

Leu Glu Ala Leu Val Gln Leu Arg Gly Arg Leu Thr Ser Gln Asp

	155	160	165
Trp Glu Arg Val His Leu Ile Val Ala Gly Gly Tyr Asp Glu Arg			
	170	175	180
Val Leu Glu Asn Val Glu His Tyr Gln Glu Leu Lys Lys Met Val			
	185	190	195
Gln Gln Ser Asp Leu Gly Gln Tyr Val Thr Phe Leu Arg Ser Phe			
	200	205	210
Ser Asp Lys Gln Lys Ile Ser Leu Leu His Ser Cys Thr Cys Val			
	215	220	225
Leu Tyr Thr Pro Ser Asn Glu His Phe Gly Ile Val Pro Leu Glu			
	230	235	240
Ala Met Tyr Met Gln Cys Pro Val Ile Ala Val Asn Ser Gly Gly			
	245	250	255
Pro Leu Glu Ser Ile Asp His Ser Val Thr Gly Phe Leu Cys Glu			
	260	265	270
Pro Asp Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Arg			
	275	280	285
Glu Pro Ser Leu Lys Ala Thr Met Gly Leu Ala Gly Arg Ala Arg			
	290	295	300
Val Lys Glu Lys Phe Ser Pro Glu Ala Phe Thr Glu Gln Leu Tyr			
	305	310	315
Arg Tyr Val Thr Lys Leu Leu Val			
	320		

<210> 211
<211> 1554
<212> DNA
<213> Homo sapiens

<400> 211
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tctacacctta tccggcttcc agacaagctg caggaattcc agggattact 150
ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtggaaag 200
tttgcatgag ttccctggta atttgcatga gagatatggg cctgtggct 250
ccttctgggtt tggcaggcgc ctcgtggta gtttggcac tgttgatgta 300
ctgaaggcgc atatcaatcc caataagaca tcggaccctt ttgaaaccat 350
gctgaagtca ttattaaggt atcaatctgg tggtggcagt gtgagtgaaa 400

accacatgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450
agtaactttg ccctcctcct aaagcttca gaagaattat tagataaaatg 500
gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgcttg 550
gttttgctat gaagtctgtt acacagatgg taatgggttag tacatttcaa 600
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ggaaaaaaca atatgaagat gccctcatgc aactggagtc tgtttaagg 750
aacatcataa aagaacgaaa aggaaggaac ttcagtcaac atattttcat 800
tgactccta gtacaaggaa accttaatga ccaacagatc ctagaagaca 850
gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc 900
tggcaatct gtttttaac cacctctgaa gaagttcaaa aaaaattata 950
tgaagagata aaccaagttt ttggaaatgg tcctgttact ccagagaaaa 1000
ttgagcagct cagatattgt cagcatgtgc tttgtgaaac tgttcgaact 1050
gccaaactga ctccagtttc tgcccagctt caagatattg aaggaaaaat 1100
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gatcggtttg atgatgaatt agtaatgaaa acttttcct cacttggatt 1250
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cagtacttct tagtgttattt gtaagagac tgcacctact ttctgtggag 1350
ggacaggta ttgaaacaaa gtagtgaactg gtaacatcat caagggaaaga 1400
agcttggatc actgtctcaa agagatatta aaattttata catttaaat 1450
cattgttaaa ttgatttggagg aaaacaacca tttaaaaaaa atctatgttg 1500
aatcctttta taaaccagta tcactttgtatataaacac ctatttgac 1550
ttaa 1554

<210> 212
<211> 462
<212> PRT
<213> Homo sapiens

<400> 212
Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu Ala Leu
1 5 10 15

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atttgtggtg tcctcatcaa ggtgattctg gataaatact acttcctctg 400
cgggcagcct ctccacttca tcccgaggaa gcagctgtgt gacggagagc 450
tggactgtcc cttggggag gacgaggagc actgtgtcaa gagttcccc 500
gaagggcctg cagtggcagt ccgcctctcc aaggaccat ccacactgca 550
ggtgctggac tcggccacag ggaactgggt ctctgcctgt ttcgacaact 600
tcacagaagc tctcgctgag acagcctgta ggcagatggg ctacagcaga 650
gctgtggaga ttggccaga ccaggatctg gatgtgttg aaatcacaga 700
aaacagccag gagttcgca tgcggaactc aagtggccc tgtctctcag 750
gctccctggc ctccctgcac tgtcttgcct gtgggaagag cctgaagacc 800
ccccgtgtgg tgggtggga ggaggcctct gtggattctt ggccttggca 850
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accccccactg ggtcctcactg gcagcccact gcttcaggaa acataccat 950
gtgttcaact ggaaggtgcg ggcaggctca gacaaactgg gcagcttccc 1000
atccctggct gtggccaaga tcatcatcat tgaattcaac cccatgtacc 1050
ccaaagacaa tgacatcgcc ctcatgaagc tgcagttccc actcaacttc 1100
tcaggcacag tcaggccat ctgtctgccc ttcttgatg aggagctcac 1150
tccagccacc ccactctgga tcattggatg gggcttacg aagcagaatg 1200
gagggaaagat gtctgacata ctgctgcagg cgtcagtcca ggtcattgac 1250
agcacacggc gcaatgcaga cgatgcgtac caggggaag tcaccgagaa 1300
gatgatgtgt gcaggcatcc cgaaaggggg tgtggacacc tgccagggtg 1350
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gtcagcagcc ctagctcgcc cacactgggt gctcccagca tcccaggag 1750
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aactttccca cactactgaa tggaagcagg ctgtcttgta aaagcccaga 1850
tcactgtggg ctggagagga gaaggaaagg gtctgcgcca gccctgtccg 1900
tcttcaccca tccccaaagcc tactagagca agaaaccagt tgtaatataa 1950
aatgcactgc cctactgttg gtatgactac cgttacctac tgggtgtcatt 2000
gttattacag ctatggccac tattattaaa gagctgtgta acatctctgg 2050
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<210> 275

<211> 432

<212> PRT

<213> Homo sapiens

<400> 275

Met Leu Gln Asp Pro Asp Ser Asp Gln Pro Leu Asn Ser Leu Asp
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Val Lys Pro Leu Arg Lys Pro Arg Ile Pro Met Glu Thr Phe Arg
20 25 30

Lys Val Gly Ile Pro Ile Ile Ala Leu Leu Ser Leu Ala Ser
35 40 45

Ile Ile Ile Val Val Leu Ile Lys Val Ile Leu Asp Lys Tyr
50 55 60

Tyr Phe Leu Cys Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln
65 70 75

Leu Cys Asp Gly Glu Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu
80 85 90

His Cys Val Lys Ser Phe Pro Glu Gly Pro Ala Val Ala Val Arg
95 100 105

Leu Ser Lys Asp Arg Ser Thr Leu Gln Val Leu Asp Ser Ala Thr
110 115 120

Gly Asn Trp Phe Ser Ala Cys Phe Asp Asn Phe Thr Glu Ala Leu
125 130 135

Ala Glu Thr Ala Cys Arg Gln Met Gly Tyr Ser Arg Ala Val Glu
140 145 150

Ile Gly Pro Asp Gln Asp Leu Asp Val Val Glu Ile Thr Glu Asn
155 160 165

Ser Gln Glu Leu Arg Met Arg Asn Ser Ser Gly Pro Cys Leu Ser
170 175 180

Gly	Ser	Leu	Val	Ser	Leu	His	Cys	Leu	Ala	Cys	Gly	Lys	Ser	Leu
185								190						195
Lys	Thr	Pro	Arg	Val	Val	Gly	Gly	Glu	Glu	Ala	Ser	Val	Asp	Ser
200								205						210
Trp	Pro	Trp	Gln	Val	Ser	Ile	Gln	Tyr	Asp	Lys	Gln	His	Val	Cys
215								220						225
Gly	Gly	Ser	Ile	Leu	Asp	Pro	His	Trp	Val	Leu	Thr	Ala	Ala	His
230								235						240
Cys	Phe	Arg	Lys	His	Thr	Asp	Val	Phe	Asn	Trp	Lys	Val	Arg	Ala
245								250						255
Gly	Ser	Asp	Lys	Leu	Gly	Ser	Phe	Pro	Ser	Leu	Ala	Val	Ala	Lys
260								265						270
Ile	Ile	Ile	Ile	Glu	Phe	Asn	Pro	Met	Tyr	Pro	Lys	Asp	Asn	Asp
275								280						285
Ile	Ala	Leu	Met	Lys	Leu	Gln	Phe	Pro	Leu	Thr	Phe	Ser	Gly	Thr
290								295						300
Val	Arg	Pro	Ile	Cys	Leu	Pro	Phe	Phe	Asp	Glu	Glu	Leu	Thr	Pro
305								310						315
Ala	Thr	Pro	Leu	Trp	Ile	Ile	Gly	Trp	Gly	Phe	Thr	Lys	Gln	Asn
320								325						330
Gly	Gly	Lys	Met	Ser	Asp	Ile	Leu	Leu	Gln	Ala	Ser	Val	Gln	Val
335								340						345
Ile	Asp	Ser	Thr	Arg	Cys	Asn	Ala	Asp	Asp	Ala	Tyr	Gln	Gly	Glu
350								355						360
Val	Thr	Glu	Lys	Met	Met	Cys	Ala	Gly	Ile	Pro	Glu	Gly	Gly	Val
365								370						375
Asp	Thr	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Met	Tyr	Gln	Ser
380								385						390
Asp	Gln	Trp	His	Val	Val	Gly	Ile	Val	Ser	Trp	Gly	Tyr	Gly	Cys
395								400						405
Gly	Gly	Pro	Ser	Thr	Pro	Gly	Val	Tyr	Thr	Lys	Val	Ser	Ala	Tyr
410								415						420
Leu	Asn	Trp	Ile	Tyr	Asn	Val	Trp	Lys	Ala	Glu	Leu			
425								430						

<210> 276
<211> 3143
<212> DNA
<213> Homo sapiens

<400> 276
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agagactgtt tatttttat taaaaatata aggctaaaaa aaa 3143

<210> 277

<211> 761

<212> PRT

<213> Homo sapiens

<400> 277

Met Ala Leu Pro Ala Leu Gly Leu Asp Pro Trp Ser Leu Leu Gly
1 5 10 15

Leu Phe Leu Phe Gln Leu Leu Gln Leu Leu Pro Thr Thr Thr
20 25 30

Ala Gly Gly Gly Gln Gly Pro Met Pro Arg Val Arg Tyr Tyr
35 40 45

Ala Gly Asp Glu Arg Arg Ala Leu Ser Phe Phe His Gln Lys Gly
50 55 60

Leu Gln Asp Phe Asp Thr Leu Leu Leu Ser Gly Asp Gly Asn Thr
65 70 75

Leu Tyr Val Gly Ala Arg Glu Ala Ile Leu Ala Leu Asp Ile Gln
80 85 90

Asp Pro Gly Val Pro Arg Leu Lys Asn Met Ile Pro Trp Pro Ala
95 100 105

Ser Asp Arg Lys Lys Ser Glu Cys Ala Phe Lys Lys Ser Asn
110 115 120

Glu Thr Gln Cys Phe Asn Phe Ile Arg Val Leu Val Ser Tyr Asn
125 130 135

Val Thr His Leu Tyr Thr Cys Gly Thr Phe Ala Phe Ser Pro Ala
140 145 150

Cys Thr Phe Ile Glu Leu Gln Asp Ser Tyr Leu Leu Pro Ile Ser
155 160 165

Glu Asp Lys Val Met Glu Gly Lys Gly Gln Ser Pro Phe Asp Pro
170 175 180

Ala His Lys His Thr Ala Val Leu Val Asp Gly Met Leu Tyr Ser
185 190 195

Gly Thr Met Asn Asn Phe Leu Gly Ser Glu Pro Ile Leu Met Arg
200 205 210

Thr Leu Gly Ser Gln Pro Val Leu Lys Thr Asp Asn Phe Leu Arg
215 220 225

Trp Leu His His Asp Ala Ser Phe Val Ala Ala Ile Pro Ser Thr
230 235 240

Gln Val Val Tyr Phe Phe Glu Glu Thr Ala Ser Glu Phe Asp
245 250 255

Phe Phe Glu Arg Leu His Thr Ser Arg Val Ala Arg Val Cys Lys
260 265 270

Asn Asp Val Gly Gly Glu Lys Leu Leu Gln Lys Lys Trp Thr Thr
275 280 285

Phe Leu Lys Ala Gln Leu Leu Cys Thr Gln Pro Gly Gln Leu Pro
290 295 300

Phe Asn Val Ile Arg His Ala Val Leu Leu Pro Ala Asp Ser Pro
305 310 315

Thr Ala Pro His Ile Tyr Ala Val Phe Thr Ser Gln Trp Gln Val
320 325 330

Gly Gly Thr Arg Ser Ser Ala Val Cys Ala Phe Ser Leu Leu Asp
335 340 345

Ile Glu Arg Val Phe Lys Gly Lys Tyr Lys Glu Leu Asn Lys Glu
350 355 360

Thr Ser Arg Trp Thr Thr Tyr Arg Gly Pro Glu Thr Asn Pro Arg
365 370 375

Pro Gly Ser Cys Ser Val Gly Pro Ser Ser Asp Lys Ala Leu Thr
380 385 390

Phe Met Lys Asp His Phe Leu Met Asp Glu Gln Val Val Gly Thr
395 400 405

Pro Leu Leu Val Lys Ser Gly Val Glu Tyr Thr Arg Leu Ala Val
410 415 420

Glu Thr Ala Gln Gly Leu Asp Gly His Ser His Leu Val Met Tyr
425 430 435

Leu Gly Thr Thr Thr Gly Ser Leu His Lys Ala Val Val Ser Gly
440 445 450

Asp Ser Ser Ala His Leu Val Glu Glu Ile Gln Leu Phe Pro Asp
455 460 465

Pro Glu Pro Val Arg Asn Leu Gln Leu Ala Pro Thr Gln Gly Ala
470 475 480

Val Phe Val Gly Phe Ser Gly Gly Val Trp Arg Val Pro Arg Ala
485 490 495

Asn Cys Ser Val Tyr Glu Ser Cys Val Asp Cys Val Leu Ala Arg
500 505 510

Asp Pro His Cys Ala Trp Asp Pro Glu Ser Arg Thr Cys Cys Leu
515 520 525

Leu Ser Ala Pro Asn Leu Asn Ser Trp Lys Gln Asp Met Glu Arg
530 535 540

Gly Asn Pro Glu Trp Ala Cys Ala Ser Gly Pro Met Ser Arg Ser
545 550 555

Leu Arg Pro Gln Ser Arg Pro Gln Ile Ile Lys Glu Val Leu Ala
560 565 570

Val Pro Asn Ser Ile Leu Glu Leu Pro Cys Pro His Leu Ser Ala
575 580 585

Leu Ala Ser Tyr Tyr Trp Ser His Gly Pro Ala Ala Val Pro Glu
590 595 600

Ala Ser Ser Thr Val Tyr Asn Gly Ser Leu Leu Leu Ile Val Gln
605 610 615

Asp Gly Val Gly Gly Leu Tyr Gln Cys Trp Ala Thr Glu Asn Gly
620 625 630

Phe Ser Tyr Pro Val Ile Ser Tyr Trp Val Asp Ser Gln Asp Gln
635 640 645

Thr Leu Ala Leu Asp Pro Glu Leu Ala Gly Ile Pro Arg Glu His
650 655 660

Val Lys Val Pro Leu Thr Arg Val Ser Gly Gly Ala Ala Leu Ala
665 670 675

Ala Gln Gln Ser Tyr Trp Pro His Phe Val Thr Val Thr Val Leu
680 685 690

Phe Ala Leu Val Leu Ser Gly Ala Leu Ile Ile Leu Val Ala Ser
695 700 705

Pro Leu Arg Ala Leu Arg Ala Arg Gly Lys Val Gln Gly Cys Glu
710 715 720

Thr Leu Arg Pro Gly Glu Lys Ala Pro Leu Ser Arg Glu Gln His
725 730 735

Leu Gln Ser Pro Lys Glu Cys Arg Thr Ser Ala Ser Asp Val Asp
740 745 750

Ala Asp Asn Asn Cys Leu Gly Thr Glu Val Ala
755 760

<210> 278
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 278
ctgctggta aatctggcgt ggag 24

<210> 279
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 279
gtctggcct ggctgtccac ccag 24

<210> 280
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 280
catcttgtca tgtacctggg aaccaccaca gggtcgtcc acaag 45

<210> 281
<211> 2320
<212> DNA
<213> Homo sapiens

<400> 281
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<210> 282

<211> 523

<212> PRT

<213> Homo sapiens

<400> 282

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Gly	Val	Leu	Leu	Ser	Glu	Ala	Ala	Lys	Ile	Leu	Thr	Ile	Ser	Thr
				20					25					30

Val	Gly	Gly	Ser	His	Tyr	Leu	Leu	Met	Asp	Arg	Val	Ser	Gln	Ile
				35				40						45

Leu	Gln	Asp	His	Gly	His	Asn	Val	Thr	Met	Leu	Asn	His	Lys	Arg
				50				55						60

Gly	Pro	Phe	Met	Pro	Asp	Phe	Lys	Lys	Glu	Glu	Lys	Ser	Tyr	Gln
			65				70							75

Val	Ile	Ser	Trp	Leu	Ala	Pro	Glu	Asp	His	Gln	Arg	Glu	Phe	Lys
			80				85							90

Lys	Ser	Phe	Asp	Phe	Phe	Leu	Glu	Glu	Thr	Leu	Gly	Gly	Arg	Gly
				95				100						105

Lys	Phe	Glu	Asn	Leu	Leu	Asn	Val	Leu	Glu	Tyr	Leu	Ala	Leu	Gln
				110				115						120

Cys	Ser	His	Phe	Leu	Asn	Arg	Lys	Asp	Ile	Met	Asp	Ser	Leu	Lys
				125				130						135

Asn	Glu	Asn	Phe	Asp	Met	Val	Ile	Val	Glu	Thr	Phe	Asp	Tyr	Cys
				140				145						150

Pro Phe Leu Ile Ala Glu Lys Leu Gly Lys Pro Phe Val Ala Ile

155 160 165
Leu Ser Thr Ser Phe Gly Ser Leu Glu Phe Gly Leu Pro Ile Pro
170 175 180
Leu Ser Tyr Val Pro Val Phe Arg Ser Leu Leu Thr Asp His Met
185 190 195
Asp Phe Trp Gly Arg Val Lys Asn Phe Leu Met Phe Phe Ser Phe
200 205 210
Cys Arg Arg Gln Gln His Met Gln Ser Thr Phe Asp Asn Thr Ile
215 220 225
Lys Glu His Phe Thr Glu Gly Ser Arg Pro Val Leu Ser His Leu
230 235 240
Leu Leu Lys Ala Glu Leu Trp Phe Ile Asn Ser Asp Phe Ala Phe
245 250 255
Asp Phe Ala Arg Pro Leu Leu Pro Asn Thr Val Tyr Val Gly Gly
260 265 270
Leu Met Glu Lys Pro Ile Lys Pro Val Pro Gln Asp Leu Glu Asn
275 280 285
Phe Ile Ala Lys Phe Gly Asp Ser Gly Phe Val Leu Val Thr Leu
290 295 300
Gly Ser Met Val Asn Thr Cys Gln Asn Pro Glu Ile Phe Lys Glu
305 310 315
Met Asn Asn Ala Phe Ala His Leu Pro Gln Gly Val Ile Trp Lys
320 325 330
Cys Gln Cys Ser His Trp Pro Lys Asp Val His Leu Ala Ala Asn
335 340 345
Val Lys Ile Val Asp Trp Leu Pro Gln Ser Asp Leu Leu Ala His
350 355 360
Pro Ser Ile Arg Leu Phe Val Thr His Gly Gly Gln Asn Ser Ile
365 370 375
Met Glu Ala Ile Gln His Gly Val Pro Met Val Gly Ile Pro Leu
380 385 390
Phe Gly Asp Gln Pro Glu Asn Met Val Arg Val Glu Ala Lys Lys
395 400 405
Phe Gly Val Ser Ile Gln Leu Lys Lys Leu Lys Ala Glu Thr Leu
410 415 420
Ala Leu Lys Met Lys Gln Ile Met Glu Asp Lys Arg Tyr Lys Ser
425 430 435
Ala Ala Val Ala Ala Ser Val Ile Leu Arg Ser His Pro Leu Ser

440 445 450
Pro Thr Gln Arg Leu Val Gly Trp Ile Asp His Val Leu Gln Thr
455 460 465
Gly Gly Ala Thr His Leu Lys Pro Tyr Val Phe Gln Gln Pro Trp
470 475 480
His Glu Gln Tyr Leu Phe Asp Val Phe Val Phe Leu Leu Gly Leu
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Thr Leu Gly Thr Leu Trp Leu Cys Gly Lys Leu Leu Gly Met Ala
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Val Trp Trp Leu Arg Gly Ala Arg Lys Val Lys Glu Thr
515 520

<210> 283
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 283
tgccttgct cacctacccc aagg 24

<210> 284
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 284
tcaggctggc ctccaaagag aggg 24

<210> 285
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 285
cccaaagatg tccacctggc tgcaaatgtg aaaattgtgg actgg 45

<210> 286
<211> 2340
<212> DNA
<213> Homo sapiens

<400> 286
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<210> 287

<211> 205

<212> PRT

<213> Homo sapiens

<400> 287

Met	Leu	Gly	Ala	Lys	Pro	His	Trp	Leu	Pro	Gly	Pro	Leu	His	Ser
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Pro	Gly	Leu	Pro	Leu	Val	Leu	Val	Leu	Leu	Ala	Leu	Gly	Ala	Gly
					20				25				30	

Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Leu	Glu	Gly	Glu	Cys
									35		40		45	

Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Ala	Gly	Gly	Pro	Gly
								50		55		60		

Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala
								65		70		75		

Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn
				80					85					90
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu
				95					100					105
Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val
					110				115					120
Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn
					125				130					135
Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val
					140				145					150
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala
					155				160					165
Thr	Ser	Ser	Val	Leu	Leu	Pro	Leu	Asp	Pro	Gly	Asp	Arg	Val	Ser
					170				175					180
Leu	Arg	Leu	Arg	Arg	Gly	Asn	Leu	Leu	Gly	Gly	Trp	Lys	Tyr	Ser
					185				190					195
Ser	Phe	Ser	Gly	Phe	Leu	Ile	Phe	Pro	Leu					
					200				205					

<210> 288

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 288

aggcagccac cagctctgtg ctac 24

<210> 289

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 289

cagagaggga agatgaggaa gccagag 27

<210> 290

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 290
ctgtgctact gcccttggac cctggggacc gagtgtctct gc 42

<210> 291
<211> 1570
<212> DNA
<213> Homo sapiens

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<210> 292
<211> 388
<212> PRT
<213> *Homo sapiens*

<400> 292
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 20 25 30
 Ala Leu Ser Arg Glu Gly Ser Gly Arg Trp Gly Thr Gly Ser Ser
 35 40 45
 Ile Leu Ser Ala Leu Gln Asp Leu Phe Ser Val Thr Trp Leu Asn
 50 55 60
 Arg Ser Lys Val Glu Lys Gln Leu Gln Val Ile Ser Val Leu Gln
 65 70 75
 Trp Val Leu Ser Phe Leu Val Leu Gly Val Ala Cys Ser Ala Ile
 80 85 90
 Leu Met Tyr Ile Phe Cys Thr Asp Cys Trp Leu Ile Ala Val Leu
 95 100 105
 Tyr Phe Thr Trp Leu Val Phe Asp Trp Asn Thr Pro Lys Lys Gly
 110 115 120
 Gly Arg Arg Ser Gln Trp Val Arg Asn Trp Ala Val Trp Arg Tyr
 125 130 135
 Phe Arg Asp Tyr Phe Pro Ile Gln Leu Val Lys Thr His Asn Leu
 140 145 150
 Leu Thr Thr Arg Asn Tyr Ile Phe Gly Tyr His Pro His Gly Ile
 155 160 165
 Met Gly Leu Gly Ala Phe Cys Asn Phe Ser Thr Glu Ala Thr Glu
 170 175 180

Val Ser Lys Lys Phe Pro Gly Ile Arg Pro Tyr Leu Ala Thr Leu
185 190 195

Ala Gly Asn Phe Arg Met Pro Val Leu Arg Glu Tyr Leu Met Ser
200 205 210

Gly Gly Ile Cys Pro Val Ser Arg Asp Thr Ile Asp Tyr Leu Leu
215 220 225

Ser Lys Asn Gly Ser Gly Asn Ala Ile Ile Val Val Gly Gly
230 235 240

Ala Ala Glu Ser Leu Ser Ser Met Pro Gly Lys Asn Ala Val Thr
245 250 255

Leu Arg Asn Arg Lys Gly Phe Val Lys Leu Ala Leu Arg His Gly
260 265 270

Ala Asp Leu Val Pro Ile Tyr Ser Phe Gly Glu Asn Glu Val Tyr
275 280 285

Lys Gln Val Ile Phe Glu Glu Gly Ser Trp Gly Arg Trp Val Gln
290 295 300

Lys Lys Phe Gln Lys Tyr Ile Gly Phe Ala Pro Cys Ile Phe His
305 310 315

Gly Arg Gly Leu Phe Ser Ser Asp Thr Trp Gly Leu Val Pro Tyr
320 325 330

Ser Lys Pro Ile Thr Thr Val Val Gly Glu Pro Ile Thr Ile Pro
335 340 345

Lys Leu Glu His Pro Thr Gln Gln Asp Ile Asp Leu Tyr His Thr
350 355 360

Met Tyr Met Glu Ala Leu Val Lys Leu Phe Asp Lys His Lys Thr
365 370 375

Lys Phe Gly Leu Pro Glu Thr Glu Val Leu Glu Val Asn
380 385

<210> 293

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 293

gctgacctgg ttcccatctta ctcc 24

<210> 294

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294
cccacagaca cccatgacac ttcc 24

<210> 295

<211> 50

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 296

<211> 3060

<212> DNA

<213> Homo sapiens

<400> 296
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aagcttcctt gacctgttagg aaggcctgtc tttaggcccgg gcacagtggc 2100
ttacacctgt aatcccagca ctttgggagg cccagacggg tggatcattt 2150
ggggtcaggc tgatctcaaa ctccctgagtt caggtgatct gccccctca 2200
gcctcccaaa gtgttgcgtat tgcaggcgtg agccactgcg cctggccgga 2250

atttctttt aaggctgaat gatgggggcc aggcacgatg gctcacgcct 2300
gtgatccaa gtagcttcca ttgtaaacat gcaccaccaat gcctggctaa 2350
ttttgtatt ttttagtagag acgtgttagc caggctggtc tcgatctcct 2400
gacctcaagt gaccacactgc ctcagcctcc caaagtactg ggattacagg 2450
cgtgagccac tgtgcctggc cttgagcatc ttgtatgtg cttattggcc 2500
atttgtatat ctcttatctt ctttgggaa atgtctgttc aagtcccttg 2550
ccttttaaa ttttattat ttatattttt atttattttt agacagggc 2600
ttgttctgtt gcccaggctg gagtacagtgc gcacagtctt ggctcaactgc 2650
agcctcgacc tcctgggctg cagtgatcct cccacactcag cctcccttgt 2700
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catgagccac tgcacctggc aaactccaa aattcaacac acacacacaa 2900
aaaaccaccc gattcaaaaat gggcagaggg gcccgggtgtg gcccccaacta 2950
ccagggagac tgaagtggga ggatcgcttgc ggcattgagaa gtcgaggctg 3000
cagtgagtcg aggttgcgc actgcattcc agcctggaca acagagttag 3050
accctgtctc 3060

<210> 297
<211> 368
<212> PRT
<213> Homo sapiens

<400> 297
Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His Leu
1 5 10 15
Leu Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn Phe
20 25 30
Val Gln Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu
35 40 45
Tyr Arg Arg Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser Gln
50 55 60
Leu Val Met Leu Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu
65 70 75
Phe Thr Asp Gln Ala Thr Val Glu Arg Phe Gly Lys Glu His Ala

	80	85	90
Val Ile Ile Leu Asn His Asn Phe Glu Ile Asp Phe Leu Cys Gly			
95	100	105	
Trp Thr Met Cys Glu Arg Phe Gly Val Leu Gly Ser Ser Lys Val			
110	115	120	
Leu Ala Lys Lys Glu Leu Leu Tyr Val Pro Leu Ile Gly Trp Thr			
125	130	135	
Trp Tyr Phe Leu Glu Ile Val Phe Cys Lys Arg Lys Trp Glu Glu			
140	145	150	
Asp Arg Asp Thr Val Val Glu Gly Leu Arg Arg Leu Ser Asp Tyr			
155	160	165	
Pro Glu Tyr Met Trp Phe Leu Leu Tyr Cys Glu Gly Thr Arg Phe			
170	175	180	
Thr Glu Thr Lys His Arg Val Ser Met Glu Val Ala Ala Ala Lys			
185	190	195	
Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro Arg Thr Lys Gly			
200	205	210	
Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val Ala Ala Val			
215	220	225	
Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser Leu			
230	235	240	
Leu Gly Ile Leu Tyr Gly Lys Tyr Glu Ala Asp Met Cys Val			
245	250	255	
Arg Arg Phe Pro Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala			
260	265	270	
Ala Gln Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln			
275	280	285	
Glu Ile Tyr Asn Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys			
290	295	300	
Pro Ala Arg Arg Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala			
305	310	315	
Thr Ile Leu Leu Ser Pro Leu Phe Ser Phe Val Leu Gly Val Phe			
320	325	330	
Ala Ser Gly Ser Pro Leu Leu Ile Leu Thr Phe Leu Gly Phe Val			
335	340	345	
Gly Ala Ala Ser Phe Gly Val Arg Arg Leu Ile Gly Glu Ser Leu			
350	355	360	
Glu Pro Gly Arg Trp Arg Leu Gln			

<210> 298
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 298
cttcctctgt gggtgacca tgtg 24

<210> 299
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 299
gccacaccttcca tgctaacgcg g 21

<210> 300
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 300
ccaaggtcct cgctaagaag gagctgctct acgtgcccct catcg 45

<210> 301
<211> 1334
<212> DNA
<213> Homo sapiens

<400> 301
gatattcttt attttaaga atctgaagta ctatgcatca ctccctccaa 50
tgtcctgggg cagccaccag gcatattcat ctttgtgtgt gttttcttt 100
tgcttagca ctggggcact tcttgcttat ttcttggta ggaaaggggc 150
tcagttgtc ttgtggggtt ggtggcaggc aggccggctt acgcctgata 200
cgccccctggg ttagaaggga agggaaagata aactttata caaatgggga 250
tagctggggt ctgagacctg cttcctcagt aaaattcctg ggatctgcct 300
ataccttctt ttctctaacc tggcataaccc tgcttaaagc ctctcagggc 350
ttctctctgt tcttaggatc aaagtattta gagctacaag agccctcatg 400

gtctggcccc tgcccccctg gccagcttca ttgtacatgt ggtgttctct 450
tgtcgttcct gtaatgtggt atgccatggg gtcttgcac aagcctttcc 500
tctttggctg gacactgttc cctgcccccc ccatactttt cctacttaat 550
atgttagtcat cctgcagatt tcaattctaa catcatttc tccagggatc 600
ctggcctgac agaatctcat ctgtttaat gctctcataa gaccacttgt 650
ttcccttttg cagcacttgc cactcagttg tatctttatg tgcgttgcgtg 700
gttgtatggg ttgtgtctgt tccccagaat gcccagctct gagctgcgtg 750
agggtcaagg gcattgtgt gcctgccagg tatagtgcct acatgtggtg 800
ggtgctcatg ttttagagac taaatggagg aggagatgag gaaaagattg 850
aaatctctca gttcaccaga tggtaggg cccagcattt taaattcaca 900
cgttgactgt gcttgtgaat tatctgggg tgcaggcctt gattcagttag 950
gcccagggtt ggcattctta acaaactccc acgtgtgtt gatgtggc 1000
ctatgaacta tactaaatag taagaatcta tggagccagg ctggcatgg 1050
tggctcacac ctatgatccc agcactttgg gaggctgagg caggctgatc 1100
acctggagtc aggattcaa gactgcctg gccaacatgg tggaaaccca 1150
tctgtactaa aaatacacaa attagctggg catggtagca catgcctgta 1200
gtcccagcta cttgggaggc tgaagcaaga gaatcgcttg aacctgggag 1250
gcggagggtt cagtgagccg agatcaggcc actgtattcc aaccagggtg 1300
acagagttag actctatgtc caaaaaaaaaaaaa 1334

<210> 302

<211> 143

<212> PRT

<213> Homo sapiens

<400> 302

Met	His	His	Ser	Leu	Gln	Cys	Pro	Gly	Ala	Ala	Thr	Arg	His	Ile
1									10					15
His	Leu	Cys	Val	Cys	Phe	Ser	Phe	Ala	Leu	Ala	Leu	Gly	His	Phe
			20						25					30
Leu	Leu	Ile	Ser	Leu	Val	Gly	Lys	Gly	Leu	Ser	Leu	Ser	Cys	Gly
									35		40			45
Val	Gly	Gly	Arg	Gln	Ala	Gly	Leu	Arg	Leu	Ile	Arg	Pro	Trp	Val
									50		55			60
Arg	Arg	Glu	Gly	Lys	Ile	Asn	Phe	Tyr	Thr	Asn	Gly	Asp	Ser	Trp

	65	70	75
Gly Leu Arg Pro Ala Ser Ser Val Lys Phe Leu Gly Ser Ala Tyr			
80	85		90
Thr Phe Phe Ser Leu Thr Trp His Thr Leu Leu Lys Ala Ser Gln			
95	100		105
Gly Phe Ser Leu Phe Leu Gly Ser Lys Tyr Leu Glu Leu Gln Glu			
110	115		120
Pro Ser Trp Ser Gly Pro Cys Pro Pro Gly Gln Leu His Cys Thr			
125	130		135
Cys Gly Val Leu Leu Ser Phe Leu			
140			

<210> 303
<211> 1768
<212> DNA
<213> Homo sapiens

<400> 303
ggctggactg gaactcctgg tcccaagtga tccacccgcc tcagcctccc 50
aaggtgctgt gattataggt gtaagccacc gtgtctggcc tctgaacaac 100
ttttcagca actaaaaaaag ccacaggagt tgaactgcta ggattctgac 150
tatgctgtgg tggcttagtgc tcctactcct acctacatta aaatctgttt 200
tttggttctct tgtaacttagc ctttaccttc ctaacacaga ggatctgtca 250
ctgtggctct ggcccaaacc tgaccttcac tctggAACGA gaacagaggt 300
ttctacccac accgtccccct cgaAGCCGGG gacagcctca ctttgctggc 350
ctctcgctgg agcagtgcgg tcaccaactg tctcacgtct ggaggcactg 400
actcgggcag tgcaggttagc tgagccttt gtagctgcg gctttcaagg 450
tgggccttgc cctggccgta gaaggattt acaagcccga agatttcata 500
ggcgatggct cccactgccc aggcatcagc cttgctgttag tcaatcactg 550
ccctggggcc aggacgggccc gtggCACACCT gtcagaAGC agtgggtgag 600
acatcacgct gcccGCCCAT ctaaccttt catgtcctgc acatcacctg 650
atccatgggc taatctgaac tctgtcccaa ggaACCCAGA gcttgagtga 700
gctgtggctc agacccagaa ggggtctgt tagaccacct gtttatgtg 750
acaggacttg cattctcctg gaacatgagg gaacGCCGGA ggAAAGCAA 800
gtggcaggga aggaacttgt gccaaattat gggTCAGAAA agatggaggt 850

gttgggttat cacaaggcat cgagtctcct gcattcagt gacatgtggg 900
ggaagggctg ccgatggcgc atgacacact cgggactcac ctctgggcc 950
atcagacaga cgttccgccc ccgatccacg taccagctgc tgaaggcata 1000
ctgcaggccc atgctctcat cagccaggca gcagccaaaa tctgcgatca 1050
ccagccaggc gcagccgtct gggaaaggagc aagcaaagt accatttctc 1100
ctccccctcct tccctctgag aggccttcct atgtccctac taaagccacc 1150
agcaagacat agctgacagg ggctaattggc tcagtggtgg cccaggaggt 1200
cagcaaggcc tgagagctga tcagaaggc ctgctgtgcg aacacggaaa 1250
tgccctccagt aagcacaggc tgcaaaatcc ccaggcaaaag gactgtgtgg 1300
ctcaatttaa atcatgttct agtaatttgg gctgtcccca agaccaaagg 1350
agctagagct tggttcaaattt gatctccaag ggcccttata ccccaggaga 1400
cttgatttg aatttggaaac cccaaatcca aacctaagaa ccaggtgcat 1450
taagaatcag ttattgccgg gtgtgggtggc ctgtaatgcc aacattttgg 1500
gaggccgagg cggtagatc acctgaggtc aggagttcaa gaccagcctg 1550
gccaacatgg taaaacccct gtctctacta aaaataaaaaaa aaaactagcc 1600
aggcatggtg gtgtgtgcct gtatcccagc tactcgggag gctgagacag 1650
gagaattact tgaacctggg aggtgaagga ggctgagaca ggagaatcac 1700
ttcagcctga gcaacacacgc gagactctgt ctcagaaaaaa ataaaaaaaaag 1750
aattatggtt atttgtaa 1768

<210> 304
<211> 109
<212> PRT
<213> Homo sapiens

<400> 304
Met Leu Trp Trp Leu Val Leu Leu Leu Pro Thr Leu Lys Ser
1 5 10 15
Val Phe Cys Ser Leu Val Thr Ser Leu Tyr Leu Pro Asn Thr Glu
20 25 30
Asp Leu Ser Leu Trp Leu Trp Pro Lys Pro Asp Leu His Ser Gly
35 40 45
Thr Arg Thr Glu Val Ser Thr His Thr Val Pro Ser Lys Pro Gly
50 55 60
Thr Ala Ser Pro Cys Trp Pro Leu Ala Gly Ala Val Pro Ser Pro

	65	70	75
Thr Val Ser Arg Leu Glu Ala Leu Thr Arg Ala Val Gln Val Ala			
80	85		90
Glu Pro Leu Gly Ser Cys Gly Phe Gln Gly Gly Pro Cys Pro Gly			
95	100		105
Arg Arg Arg Asp			

<210> 305
<211> 989
<212> DNA
<213> Homo sapiens

<400> 305
gcggggccgc gagtccgaga cctgtcccag gagctccagc tcacgtgacc 50
tgtcaactgcc tccccccgc tcctgcccgc gccatgaccc agccggtgcc 100
ccggctctcc gtcccccccg cgctggccct gggctcagcc gcactggcg 150
ccgccttcgc cactggcctc ttccctggga ggcggtgccc cccatggcga 200
ggccggcgag agcagtgcct gcttccccc gaggacagcc gcctgtggca 250
gtatcttctg agccgctcca tgccggagca cccggcgctg cgaaggctga 300
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caggcccagc tcttggccaa cctggcgccg ctcatccagg ccaagaaggc 400
gctggacactg ggcacattca cgggctactc cgccctggcc ctggccctgg 450
cgctgcccgc ggacgggcgc gtgggtaccc gcggaggtgga cgccgcagccc 500
ccggagctgg gacggccct gtggaggcag gccgaggcgg agcacaagat 550
cgacctccgg ctgaagcccg cttggagac cctggacgag ctgctggcgg 600
cgggcgaggc cgacccatcc gacgtggccg tgggtggatgc ggacaaggag 650
aactgctccg cctactacga gcgcgtgcctg cagctgctgc gacccggagg 700
catcctcgcc gtcctcagag tcctgtggcg cgggaagggtg ctgcaacctc 750
cggaaaggggc cgtggcgcc gagtggtgc gaaacctaaa cgaacgcatac 800
cgccgggacg tcagggtcta catcagcctc ctggccctgg gcgtggact 850
caccttggcc ttcaagatct agggctggcc cctagtgagt gggctcgagg 900
gagggttgcc tggaaacccc aggaattgac cctgagttt aaattcgaaa 950
ataaagtggg gctggacac aaaaaaaaaa aaaaaaaaaa 989

<210> 306
<211> 262
<212> PRT
<213> Homo sapiens

<400> 306
Met Thr Gln Pro Val Pro Arg Leu Ser Val Pro Ala Ala Leu Ala
1 5 10 15

Leu Gly Ser Ala Ala Leu Gly Ala Ala Phe Ala Thr Gly Leu Phe
20 25 30

Leu Gly Arg Arg Cys Pro Pro Trp Arg Gly Arg Arg Glu Gln Cys
35 40 45

Leu Leu Pro Pro Glu Asp Ser Arg Leu Trp Gln Tyr Leu Leu Ser
50 55 60

Arg Ser Met Arg Glu His Pro Ala Leu Arg Ser Leu Arg Leu Leu
65 70 75

Thr Leu Glu Gln Pro Gln Gly Asp Ser Met Met Thr Cys Glu Gln
80 85 90

Ala Gln Leu Leu Ala Asn Leu Ala Arg Leu Ile Gln Ala Lys Lys
95 100 105

Ala Leu Asp Leu Gly Thr Phe Thr Gly Tyr Ser Ala Leu Ala Leu
110 115 120

Ala Leu Ala Leu Pro Ala Asp Gly Arg Val Val Thr Cys Glu Val
125 130 135

Asp Ala Gln Pro Pro Glu Leu Gly Arg Pro Leu Trp Arg Gln Ala
140 145 150

Glu Ala Glu His Lys Ile Asp Leu Arg Leu Lys Pro Ala Leu Glu
155 160 165

Thr Leu Asp Glu Leu Leu Ala Ala Gly Glu Ala Gly Thr Phe Asp
170 175 180

Val Ala Val Val Asp Ala Asp Lys Glu Asn Cys Ser Ala Tyr Tyr
185 190 195

Glu Arg Cys Leu Gln Leu Leu Arg Pro Gly Gly Ile Leu Ala Val
200 205 210

Leu Arg Val Leu Trp Arg Gly Lys Val Leu Gln Pro Pro Lys Gly
215 220 225

Asp Val Ala Ala Glu Cys Val Arg Asn Leu Asn Glu Arg Ile Arg
230 235 240

Arg Asp Val Arg Val Tyr Ile Ser Leu Leu Pro Leu Gly Asp Gly
245 250 255

Leu Thr Leu Ala Phe Lys Ile
260

<210> 307
<211> 2272
<212> DNA
<213> Homo sapiens

<400> 307
ccggcgcgc agccgctacc gccgctgcag ccgcattccg cggcctggc 50
ctctcgccgt cagcatgcca cacgcattca agcccggga cttggtgttc 100
gctaagatga agggctaccc tcactggcct gccaggatcg acgacatcgc 150
ggatggcgcc gtgaagcccc cacccaaaca gtaccccatc ttttcttg 200
gcacacacga aacagcattc ctgggaccga aggacctgtt cccctacgac 250
aaatgtaaag acaagtacgg gaagcccaac aagaggaaag gttcaatga 300
aggcgtgtgg gagatccaga acaacccca cgccagctac agcgccctc 350
cgccagttagt ctcctccgac agcgaggccc ccgaggccaa cccgcccac 400
ggcagttagt ctgacgagga cgatgaggac cgggggtca tggccgtcac 450
agcggttaacc gccacagctg ccagcgacag gatggagagc gactcagact 500
cagacaagag tagcgacaaac agtggcctga agaggaagac gcctgcgccta 550
aagatgtcggtctcgaaac agcccgaaag gcctccagcg acctggatca 600
ggccagcgtg tccccatccg aagaggagaa ctggaaagc tcatactgagt 650
cgagaagac cagcgaccag gacttcacac ctgagaagaa agcagcggc 700
cggcgccac ggaggggccc tctgggggg cggaaaaaaa agaaggcgcc 750
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tcctccgact ccgatgtgtc tgtgaagaag cctccgaggg gcaggaagcc 900
agcggagaag cctctcccgaa agcccgagg gcccggaccg aagcctgaac 950
ggcctccgtc cagctccagc agtgacagtg acagcgacga ggtggaccgc 1000
atcagttagt ggaagcggcg ggacgaggcg cggaggcgagc agctggaggc 1050
ccggcgccgg cgagagcagg aggaggagct cggccgcctg cgggagcagg 1100
agaaggagga gaaggagcgg aggcgcgagc gggccgaccg cggggaggct 1150
gagcggggca gcccggcagc cagcggggac gagctcaggaggc 1200

gcccgtcaag aagcggggac gcaaggcccg gggccggggt cccccgtcct 1250
cctctgactc cgagcccgag gccgagctgg agagagaggc caagaaatca 1300
gcgaagaagc cgcatcctc aagcacagag cccgcccagga aacctggcca 1350
gaaggagaag agagtgcggc ccgaggagaa gcaacaagcc aagccgtga 1400
aggtagggcg gacccggaag cggtccgagg gcttctcgat ggacaggaag 1450
gtagagaaga agaaagagcc ctccgtggag gagaagctgc agaagctgca 1500
cagttagatc aagtttgcac taaaggtcga cagccggac gtgaagaggt 1550
gcctgaatgc cctagaggag ctggaaaccc tgcaggtgac ctctcagatc 1600
ctccagaaga acacagacgt ggtggccacc ttgaagaaga ttgcgggtta 1650
caaagcgaac aaggacgtaa tggagaaggc agcagaagtc tataccggc 1700
tcaagtgcgc ggtcctcgcc ccaaagatcg aggccgtgca gaaagtgaac 1750
aaggctggaa tggagaagga gaaggccgag gagaagctgg ccggggagga 1800
gctggccggg gaggaggccc cccaggagaa ggcggaggac aagcccagca 1850
ccgatctctc agccccagtg aatggcgagg ccacatcaca gaagggggag 1900
agcgcagagg acaaggagca cgaggagggt cggactcgg aggaggggcc 1950
aagggtgtggc tcctctgaag acctgcacga cagcgtacgg gagggtcccc 2000
acctggacag gcctggagc gaccggcagg agcgcgagag ggcacgggg 2050
gactcgagg ccctggacga ggagagctga gccgcgggca gccaggccc 2100
gccccccccc gagctcaggc tgccccctc cttccccggc tcgcaggaga 2150
gcagagcaga gaactgtggg gaacgctgtg ctgttgttat ttgttccctt 2200
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actataaacg gtttttaat ga 2272

<210> 308

<211> 671

<212> PRT

<213> Homo sapiens

<400> 308

Met	Pro	His	Ala	Phe	Lys	Pro	Gly	Asp	Leu	Val	Phe	Ala	Lys	Met
1														15

Lys	Gly	Tyr	Pro	His	Trp	Pro	Ala	Arg	Ile	Asp	Asp	Ile	Ala	Asp
														30

Gly Ala Val Lys Pro Pro Pro Asn Lys Tyr Pro Ile Phe Phe Phe

35	40	45
Gly Thr His Glu Thr Ala Phe Leu Gly Pro Lys Asp Leu Phe Pro		
50	55	60
Tyr Asp Lys Cys Lys Asp Lys Tyr Gly Lys Pro Asn Lys Arg Lys		
65	70	75
Gly Phe Asn Glu Gly Leu Trp Glu Ile Gln Asn Asn Pro His Ala		
80	85	90
Ser Tyr Ser Ala Pro Pro Val Ser Ser Asp Ser Glu Ala		
95	100	105
Pro Glu Ala Asn Pro Ala Asp Gly Ser Asp Ala Asp Glu Asp Asp		
110	115	120
Glu Asp Arg Gly Val Met Ala Val Thr Ala Val Thr Ala Thr Ala		
125	130	135
Ala Ser Asp Arg Met Glu Ser Asp Ser Asp Ser Asp Lys Ser Ser		
140	145	150
Asp Asn Ser Gly Leu Lys Arg Lys Thr Pro Ala Leu Lys Met Ser		
155	160	165
Val Ser Lys Arg Ala Arg Lys Ala Ser Ser Asp Leu Asp Gln Ala		
170	175	180
Ser Val Ser Pro Ser Glu Glu Asn Ser Glu Ser Ser Ser Glu		
185	190	195
Ser Glu Lys Thr Ser Asp Gln Asp Phe Thr Pro Glu Lys Lys Ala		
200	205	210
Ala Val Arg Ala Pro Arg Arg Gly Pro Leu Gly Gly Arg Lys Lys		
215	220	225
Lys Lys Ala Pro Ser Ala Ser Asp Ser Asp Ser Lys Ala Asp Ser		
230	235	240
Asp Gly Ala Lys Pro Glu Pro Val Ala Met Ala Arg Ser Ala Ser		
245	250	255
Ser Ser Ser Ser Ser Ser Ser Asp Ser Asp Val Ser Val		
260	265	270
Lys Lys Pro Pro Arg Gly Arg Lys Pro Ala Glu Lys Pro Leu Pro		
275	280	285
Lys Pro Arg Gly Arg Lys Pro Lys Pro Glu Arg Pro Pro Ser Ser		
290	295	300
Ser Ser Ser Asp Ser Asp Ser Asp Glu Val Asp Arg Ile Ser Glu		
305	310	315
Trp Lys Arg Arg Asp Glu Ala Arg Arg Glu Leu Glu Ala Arg		

320 325 330
Arg Arg Arg Glu Gln Glu Glu Glu Leu Arg Arg Leu Arg Glu Gln
335 340 345
Glu Lys Glu Glu Lys Glu Arg Arg Arg Glu Arg Ala Asp Arg Gly
350 355 360
Glu Ala Glu Arg Gly Ser Gly Gly Ser Ser Gly Asp Glu Leu Arg
365 370 375
Glu Asp Asp Glu Pro Val Lys Lys Arg Gly Arg Lys Gly Arg Gly
380 385 390
Arg Gly Pro Pro Ser Ser Ser Asp Ser Glu Pro Glu Ala Glu Leu
395 400 405
Glu Arg Glu Ala Lys Lys Ser Ala Lys Lys Pro Gln Ser Ser Ser
410 415 420
Thr Glu Pro Ala Arg Lys Pro Gly Gln Lys Glu Lys Arg Val Arg
425 430 435
Pro Glu Glu Lys Gln Gln Ala Lys Pro Val Lys Val Glu Arg Thr
440 445 450
Arg Lys Arg Ser Glu Gly Phe Ser Met Asp Arg Lys Val Glu Lys
455 460 465
Lys Lys Glu Pro Ser Val Glu Glu Lys Leu Gln Lys Leu His Ser
470 475 480
Glu Ile Lys Phe Ala Leu Lys Val Asp Ser Pro Asp Val Lys Arg
485 490 495
Cys Leu Asn Ala Leu Glu Glu Leu Gly Thr Leu Gln Val Thr Ser
500 505 510
Gln Ile Leu Gln Lys Asn Thr Asp Val Val Ala Thr Leu Lys Lys
515 520 525
Ile Arg Arg Tyr Lys Ala Asn Lys Asp Val Met Glu Lys Ala Ala
530 535 540
Glu Val Tyr Thr Arg Leu Lys Ser Arg Val Leu Gly Pro Lys Ile
545 550 555
Glu Ala Val Gln Lys Val Asn Lys Ala Gly Met Glu Lys Glu Lys
560 565 570
Ala Glu Glu Lys Leu Ala Gly Glu Glu Leu Ala Gly Glu Glu Ala
575 580 585
Pro Gln Glu Lys Ala Glu Asp Lys Pro Ser Thr Asp Leu Ser Ala
590 595 600
Pro Val Asn Gly Glu Ala Thr Ser Gln Lys Gly Glu Ser Ala Glu

	605	610	615
Asp Lys Glu His Glu Glu Gly Arg Asp Ser Glu Glu Gly Pro Arg			
	620	625	630
Cys Gly Ser Ser Glu Asp Leu His Asp Ser Val Arg Glu Gly Pro			
	635	640	645
Asp Leu Asp Arg Pro Gly Ser Asp Arg Gln Glu Arg Glu Arg Ala			
	650	655	660
Arg Gly Asp Ser Glu Ala Leu Asp Glu Glu Ser			
	665	670	

<210> 309
<211> 3871
<212> DNA
<213> Homo sapiens

<400> 309
gttggttctc ctggatcttc accttaccaa ctgcagatct tgggactcat 50
cagcctcaat aattatatta aattaacacc atttgaaga gaacatttt 100
ttccatcatga atgctaataa agatgaaaga cttaaagcca gaagccaaga 150
tttcacctt ttccctgctt tcatgtatgc aagcatgacc atgttgttc 200
ttccagtcac tggcacttg aagcaaaata ttccaagact caagctaacc 250
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<211> 777

<212> PRT

<213> Homo sapiens

<400> 310

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Phe Leu Pro Val Thr Gly Thr Leu Lys Gln Asn Ile Pro Arg Leu
35 40 45

Lys Leu Thr Tyr Lys Asp Leu Leu Leu Ser Asn Ser Cys Ile Pro
50 55 60

Phe Leu Gly Ser Ser Glu Gly Leu Asp Phe Gln Thr Leu Leu Leu
65 70 75

Asp Glu Glu Arg Gly Arg Leu Leu Leu Gly Ala Lys Asp His Ile
80 85 90

Phe Leu Leu Ser Leu Val Asp Leu Asn Lys Asn Phe Lys Lys Ile
95 100 105

Tyr Trp Pro Ala Ala Lys Glu Arg Val Glu Leu Cys Lys Leu Ala
110 115 120

Gly Lys Asp Ala Asn Thr Glu Cys Ala Asn Phe Ile Arg Val Leu
125 130 135

Gln Pro Tyr Asn Lys Thr His Ile Tyr Val Cys Gly Thr Gly Ala
140 145 150

Phe His Pro Ile Cys Gly Tyr Ile Asp Leu Gly Val Tyr Lys Glu
155 160 165

Asp Ile Ile Phe Lys Leu Asp Thr His Asn Leu Glu Ser Gly Arg
170 175 180

Leu Lys Cys Pro Phe Asp Pro Gln Gln Pro Phe Ala Ser Val Met
185 190 195

Thr Asp Glu Tyr Leu Tyr Ser Gly Thr Ala Ser Asp Phe Leu Gly
200 205 210

Lys Asp Thr Ala Phe Thr Arg Ser Leu Gly Pro Thr His Asp His
215 220 225

His Tyr Ile Arg Thr Asp Ile Ser Glu His Tyr Trp Leu Asn Gly

230 235 240
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245 250 255
Asp Asp Asp Lys Ile Tyr Phe Phe Arg Glu Ser Ser Gln Glu
260 265 270
Gly Ser Thr Ser Asp Lys Thr Ile Leu Ser Arg Val Gly Arg Val
275 280 285
Cys Lys Asn Asp Val Gly Gln Arg Ser Leu Ile Asn Lys Trp
290 295 300
Thr Thr Phe Leu Lys Ala Arg Leu Ile Cys Ser Ile Pro Gly Ser
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Asp Gly Ala Asp Thr Tyr Phe Asp Glu Leu Gln Asp Ile Tyr Leu
320 325 330
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335 340 345
Thr Thr Thr Ser Ser Ile Phe Lys Gly Ser Ala Val Cys Val Tyr
350 355 360
Ser Met Ala Asp Ile Arg Ala Val Phe Asn Gly Pro Tyr Ala His
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Lys Glu Ser Ala Asp His Arg Trp Val Gln Tyr Asp Gly Arg Ile
380 385 390
Pro Tyr Pro Arg Pro Gly Thr Cys Pro Ser Lys Thr Tyr Asp Pro
395 400 405
Leu Ile Lys Ser Thr Arg Asp Phe Pro Asp Asp Val Ile Ser Phe
410 415 420
Ile Lys Arg His Ser Val Met Tyr Lys Ser Val Tyr Pro Val Ala
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Gly Gly Pro Thr Phe Lys Arg Ile Asn Val Asp Tyr Arg Leu Thr
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Gln Ile Val Val Asp His Val Ile Ala Glu Asp Gly Gln Tyr Asp
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470 475 480
Ser Ile Ser Lys Glu Lys Trp Asn Met Glu Glu Val Val Leu Glu
485 490 495
Glu Leu Gln Ile Phe Lys His Ser Ser Ile Ile Leu Asn Met Glu
500 505 510
Leu Ser Leu Lys Gln Gln Gln Leu Tyr Ile Gly Ser Arg Asp Gly

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Cys Ala Asp Cys Cys Leu Ala Arg Asp Pro Tyr Cys Ala Trp Asp		
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Gly Asn Ala Cys Ser Arg Tyr Ala Pro Thr Ser Lys Arg Arg Ala		
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Arg Arg Gln Asp Val Lys Tyr Gly Asp Pro Ile Thr Gln Cys Trp		
575	580	585
Asp Ile Glu Asp Ser Ile Ser His Glu Thr Ala Asp Glu Lys Val		
590	595	600
Ile Phe Gly Ile Glu Phe Asn Ser Thr Phe Leu Glu Cys Ile Pro		
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Lys Ser Gln Gln Ala Thr Ile Lys Trp Tyr Ile Gln Arg Ser Gly		
620	625	630
Asp Glu His Arg Glu Glu Leu Lys Pro Asp Glu Arg Ile Ile Lys		
635	640	645
Thr Glu Tyr Gly Leu Leu Ile Arg Ser Leu Gln Lys Lys Asp Ser		
650	655	660
Gly Met Tyr Tyr Cys Lys Ala Gln Glu His Thr Phe Ile His Thr		
665	670	675
Ile Val Lys Leu Thr Leu Asn Val Ile Glu Asn Glu Gln Met Glu		
680	685	690
Asn Thr Gln Arg Ala Glu His Glu Glu Gly Gln Val Lys Asp Leu		
695	700	705
Leu Ala Glu Ser Arg Leu Arg Tyr Lys Asp Tyr Ile Gln Ile Leu		
710	715	720
Ser Ser Pro Asn Phe Ser Leu Asp Gln Tyr Cys Glu Gln Met Trp		
725	730	735
His Arg Glu Lys Arg Arg Gln Arg Asn Lys Gly Gly Pro Lys Trp		
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Lys His Met Gln Glu Met Lys Lys Arg Asn Arg Arg His His		
755	760	765
Arg Asp Leu Asp Glu Leu Pro Arg Ala Val Ala Thr		
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<211> 25

<212> DNA

<213> Artificial Sequence

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<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 312
gcttggacat gtaccaggcc gtgg 24

<210> 313
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<211> 3934
<212> DNA
<213> Homo sapiens

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<211> 370

<212> PRT

<213> Homo sapiens

<400> 315

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Val Phe Pro Pro Thr Pro Val Leu Cys Leu Pro Asn Gln Val Leu
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Gln Arg Leu Glu Gln Arg Arg Gln Gln Ala Ser Glu Arg Glu Ala
35 40 45

Pro Ser Ile Glu Gln Arg Leu Gln Glu Val Arg Glu Ser Ile Arg
50 55 60

Arg Ala Gln Val Ser Gln Val Lys Gly Ala Ala Arg Leu Ala Leu
65 70 75

Leu Gln Gly Ala Gly Leu Asp Val Glu Arg Trp Leu Lys Pro Ala
80 85 90

Met Thr Gln Ala Gln Asp Glu Val Glu Gln Glu Arg Arg Leu Ser
95 100 105

Glu Ala Arg Leu Ser Gln Arg Asp Leu Ser Pro Thr Ala Glu Asp
110 115 120

Ala Glu Leu Ser Asp Phe Glu Glu Cys Glu Glu Thr Gly Glu Leu
125 130 135

Phe Glu Glu Pro Ala Pro Gln Ala Leu Ala Thr Arg Ala Leu Pro
140 145 150

Cys Pro Ala His Val Val Phe Arg Tyr Gln Ala Gly Arg Glu Asp
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Glu Leu Thr Ile Thr Glu Gly Glu Trp Leu Glu Val Ile Glu Glu
170 175 180

Gly Asp Ala Asp Glu Trp Val Lys Ala Arg Asn Gln His Gly Glu
185 190 195

Val Gly Phe Val Pro Glu Arg Tyr Leu Asn Phe Pro Asp Leu Ser
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Leu Pro Glu Ser Ser Gln Asp Ser Asp Asn Pro Cys Gly Ala Glu
215 220 225

Pro Thr Ala Phe Leu Ala Gln Ala Leu Tyr Ser Tyr Thr Gly Gln
230 235 240

Ser Ala Glu Glu Leu Ser Phe Pro Glu Gly Ala Leu Ile Arg Leu
245 250 255

Leu Pro Arg Ala Gln Asp Gly Val Asp Asp Gly Phe Trp Arg Gly
260 265 270

Glu Phe Gly Gly Arg Val Gly Val Phe Pro Ser Leu Leu Val Glu
275 280 285

Glu Leu Leu Gly Pro Pro Gly Pro Pro Glu Leu Ser Asp Pro Glu
290 295 300

Gln Met Leu Pro Ser Pro Ser Pro Pro Ser Phe Ser Pro Pro Ala
305 310 315

Pro Thr Ser Val Leu Asp Gly Pro Pro Ala Pro Val Leu Pro Gly
320 325 330

Asp Lys Ala Leu Asp Phe Pro Gly Phe Leu Asp Met Met Ala Pro
335 340 345

Arg Leu Arg Pro Met Arg Pro Pro Pro Pro Pro Ala Lys Ala
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Pro Asp Pro Gly His Pro Asp Pro Leu Thr
365 370

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<211> 4407
<212> DNA
<213> Homo sapiens

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cctgcccctgg gaggcagtga tgggttagtg gatggaaggg gctgacagac 3150
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cactttattt tagcaccagg gaaggggaca aggactaggg tcctgggaa 3300
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tggccaggct gctcttgaac tcctgacctc aggtaatcga cctgcctcgg 4100
cctcccaaag tgctgggatt acaggtgtga gccaccacgc ccgtacata 4150
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atgtggttgc atcctaactc catgtctctg agcattagat ttctcatttg 4250
ccaataataa tacctccctt agaagttgt tgtgaggatt aaataatgta 4300
aataaagaac tagcataaca ctcaaaaaaaaaaaaaaaaaaaaaaaa 4350
aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa 4400

aaggaaa 4407

<210> 317

<211> 837

<212> PRT

<213> Homo sapiens

<400> 317

Met Ser Gln Thr Gly Ser His Pro Gly Arg Gly Leu Ala Gly Arg
1 5 10 15

Trp Leu Trp Gly Ala Gln Pro Cys Leu Leu Leu Pro Ile Val Pro
20 25 30

Leu Ser Trp Leu Val Trp Leu Leu Leu Leu Leu Ala Ser Leu
35 40 45

Leu Pro Ser Ala Arg Leu Ala Ser Pro Leu Pro Arg Glu Glu Glu
50 55 60

Ile Val Phe Pro Glu Lys Leu Asn Gly Ser Val Leu Pro Gly Ser
65 70 75

Gly Ala Pro Ala Arg Leu Leu Cys Arg Leu Gln Ala Phe Gly Glu
80 85 90

Thr Leu Leu Leu Glu Leu Glu Gln Asp Ser Gly Val Gln Val Glu
95 100 105

Gly Leu Thr Val Gln Tyr Leu Gly Gln Ala Pro Glu Leu Leu Gly
110 115 120

Gly Ala Glu Pro Gly Thr Tyr Leu Thr Gly Thr Ile Asn Gly Asp
125 130 135

Pro Glu Ser Val Ala Ser Leu His Trp Asp Gly Gly Ala Leu Leu
140 145 150

Gly Val Leu Gln Tyr Arg Gly Ala Glu Leu His Leu Gln Pro Leu
155 160 165

Glu Gly Gly Thr Pro Asn Ser Ala Gly Gly Pro Gly Ala His Ile
170 175 180

Leu Arg Arg Lys Ser Pro Ala Ser Gly Gln Gly Pro Met Cys Asn
185 190 195

Val Lys Ala Pro Leu Gly Ser Pro Ser Pro Arg Pro Arg Arg Ala
200 205 210

Lys Arg Phe Ala Ser Leu Ser Arg Phe Val Glu Thr Leu Val Val
215 220 225

Ala Asp Asp Lys Met Ala Ala Phe His Gly Ala Gly Leu Lys Arg
230 235 240

Tyr Leu Leu Thr Val Met Ala Ala Ala Lys Ala Phe Lys His

245 250 255
Pro Ser Ile Arg Asn Pro Val Ser Leu Val Val Thr Arg Leu Val
260 265 270
Ile Leu Gly Ser Gly Glu Glu Gly Pro Gln Val Gly Pro Ser Ala
275 280 285
Ala Gln Thr Leu Arg Ser Phe Cys Ala Trp Gln Arg Gly Leu Asn
290 295 300
Thr Pro Glu Asp Ser Gly Pro Asp His Phe Asp Thr Ala Ile Leu
305 310 315
Phe Thr Arg Gln Asp Leu Cys Gly Val Ser Thr Cys Asp Thr Leu
320 325 330
Gly Met Ala Asp Val Gly Thr Val Cys Asp Pro Ala Arg Ser Cys
335 340 345
Ala Ile Val Glu Asp Asp Gly Leu Gln Ser Ala Phe Thr Ala Ala
350 355 360
His Glu Leu Gly His Val Phe Asn Met Leu His Asp Asn Ser Lys
365 370 375
Pro Cys Ile Ser Leu Asn Gly Pro Leu Ser Thr Ser Arg His Val
380 385 390
Met Ala Pro Val Met Ala His Val Asp Pro Glu Glu Pro Trp Ser
395 400 405
Pro Cys Ser Ala Arg Phe Ile Thr Asp Phe Leu Asp Asn Gly Tyr
410 415 420
Gly His Cys Leu Leu Asp Lys Pro Glu Ala Pro Leu His Leu Pro
425 430 435
Val Thr Phe Pro Gly Lys Asp Tyr Asp Ala Asp Arg Gln Cys Gln
440 445 450
Leu Thr Phe Gly Pro Asp Ser Arg His Cys Pro Gln Leu Pro Pro
455 460 465
Pro Cys Ala Ala Leu Trp Cys Ser Gly His Leu Asn Gly His Ala
470 475 480
Met Cys Gln Thr Lys His Ser Pro Trp Ala Asp Gly Thr Pro Cys
485 490 495
Gly Pro Ala Gln Ala Cys Met Gly Gly Arg Cys Leu His Met Asp
500 505 510
Gln Leu Gln Asp Phe Asn Ile Pro Gln Ala Gly Gly Trp Gly Pro
515 520 525
Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Val

530 535 540
Gln Phe Ser Ser Arg Asp Cys Thr Arg Pro Val Pro Arg Asn Gly
545 550 555
Gly Lys Tyr Cys Glu Gly Arg Arg Thr Arg Phe Arg Ser Cys Asn
560 565 570
Thr Glu Asp Cys Pro Thr Gly Ser Ala Leu Thr Phe Arg Glu Glu
575 580 585
Gln Cys Ala Ala Tyr Asn His Arg Thr Asp Leu Phe Lys Ser Phe
590 595 600
Pro Gly Pro Met Asp Trp Val Pro Arg Tyr Thr Gly Val Ala Pro
605 610 615
Gln Asp Gln Cys Lys Leu Thr Cys Gln Ala Arg Ala Leu Gly Tyr
620 625 630
Tyr Tyr Val Leu Glu Pro Arg Val Val Asp Gly Thr Pro Cys Ser
635 640 645
Pro Asp Ser Ser Ser Val Cys Val Gln Gly Arg Cys Ile His Ala
650 655 660
Gly Cys Asp Arg Ile Ile Gly Ser Lys Lys Lys Phe Asp Lys Cys
665 670 675
Met Val Cys Gly Gly Asp Gly Ser Gly Cys Ser Lys Gln Ser Gly
680 685 690
Ser Phe Arg Lys Phe Arg Tyr Gly Tyr Asn Asn Val Val Thr Ile
695 700 705
Pro Ala Gly Ala Thr His Ile Leu Val Arg Gln Gln Gly Asn Pro
710 715 720
Gly His Arg Ser Ile Tyr Leu Ala Leu Lys Leu Pro Asp Gly Ser
725 730 735
Tyr Ala Leu Asn Gly Glu Tyr Thr Leu Met Pro Ser Pro Thr Asp
740 745 750
Val Val Leu Pro Gly Ala Val Ser Leu Arg Tyr Ser Gly Ala Thr
755 760 765
Ala Ala Ser Glu Thr Leu Ser Gly His Gly Pro Leu Ala Gln Pro
770 775 780
Leu Thr Leu Gln Val Leu Val Ala Gly Asn Pro Gln Asp Thr Arg
785 790 795
Leu Arg Tyr Ser Phe Phe Val Pro Arg Pro Thr Pro Ser Thr Pro
800 805 810
Arg Pro Thr Pro Gln Asp Trp Leu His Arg Arg Ala Gln Ile Leu

815 820 825

Glu Ile Leu Arg Arg Arg Pro Trp Ala Gly Arg Lys
 830 835

<210> 318
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 318
ccctgaagct gccagatggc tcc 23

<210> 319
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 319
ctgtgctttt cggtgcagcc agtc 24

<210> 320
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 320
ccacagatgt ggtactgcct ggggcagtca gttgcgccta cag 43

<210> 321
<211> 1197
<212> DNA
<213> Homo sapiens

<400> 321
cagcagtggc ctctcagtcc tctcaaagca aggaaagagt actgtgtgct 50
gagagaccat ggcaaagaat cctccagaga atttgtaaga ctgtcacatt 100
ctaaatgcag aagcttttaa atccaagaaa atatgtaaat cacttaagat 150
ttgtggactg gtgtttggta tcctggccct aactctaatt gtcctgttt 200
gggggagcaa gcacttctgg ccggaggtac ccaaaaaagc ctatgacatg 250
gagcacactt tctacagcaa tggagagaag aagaagattt acatggaaat 300
tgatcctgtg accagaactg aaatattcag aagcgaaat ggcactgtg 350

aaacattgga agtgcacgac tttaaaaacg gatacactgg catctacttc 400
gtgggtcttc aaaatgttt tatcaaaact cagattaaag tgattcctga 450
attttctgaa ccagaagagg aaatagatga gaatgaagaa attaccacaa 500
cttccttga acagtcaatc atttgggtcc cagcagaaaa gcctattgaa 550
aaccgagatt ttcttaaaaa ttccaaaatt ctggagattt gtgataacgt 600
gaccatgtat tggatcaatc ccactctaattt atcagttct gagttacaag 650
actttgagga ggagggagaa gatcttcaact ttcctgccaa cgaaaaaaaa 700
gggattgaac aaaatgaaca gtgggtggc cctcaagtga aagtagagaa 750
gaccgcgtcac gccagacaag caagtgagga agaacttcca ataaatgact 800
atactgaaaa tggaatagaa tttgatccc tgctggatga gagaggttat 850
tgttgtatTTT actgccgtcg aggcaaccgc tattggccgc gcgtctgtga 900
acctttacta ggctactacc catatccata ctgctaccaa ggaggacgag 950
tcatctgtcg tgtcatcatg ccttgtaact ggtgggtggc ccgcattgtg 1000
gggagggtct aataggaggt ttgagctcaa atgcttaaac tgctggcaac 1050
atataataaa tgcatttat tcaatgaatt tctgcctatg aggcatctgg 1100
ccccctggtag ccagctctcc agaattactt gtaggtaatt cctctttca 1150
tgttctaata aacttctaca ttatcaccaa aaaaaaaaaa aaaaaaaaa 1197

<210> 322
<211> 317
<212> PRT
<213> Homo sapiens

<400> 322
Met Ala Lys Asn Pro Pro Glu Asn Cys Glu Asp Cys His Ile Leu
1 5 10 15
Asn Ala Glu Ala Phe Lys Ser Lys Ile Cys Lys Ser Leu Lys
20 25 30
Ile Cys Gly Leu Val Phe Gly Ile Leu Ala Leu Thr Leu Ile Val
35 40 45
Leu Phe Trp Gly Ser Lys His Phe Trp Pro Glu Val Pro Lys Lys
50 55 60
Ala Tyr Asp Met Glu His Thr Phe Tyr Ser Asn Gly Glu Lys Lys
65 70 75
Lys Ile Tyr Met Glu Ile Asp Pro Val Thr Arg Thr Glu Ile Phe

80	85	90
Arg Ser Gly Asn Gly Thr Asp Glu Thr	Leu Glu Val His Asp Phe	
95	100	105
Lys Asn Gly Tyr Thr Gly Ile Tyr Phe Val	Gly Leu Gln Lys Cys	
110	115	120
Phe Ile Lys Thr Gln Ile Lys Val Ile Pro	Glu Phe Ser Glu Pro	
125	130	135
Glu Glu Glu Ile Asp Glu Asn Glu Glu	Ile Thr Thr Thr Phe Phe	
140	145	150
Glu Gln Ser Val Ile Trp Val Pro Ala	Glu Lys Pro Ile Glu Asn	
155	160	165
Arg Asp Phe Leu Lys Asn Ser Lys Ile	Leu Glu Ile Cys Asp Asn	
170	175	180
Val Thr Met Tyr Trp Ile Asn Pro Thr	Leu Ile Ser Val Ser Glu	
185	190	195
Leu Gln Asp Phe Glu Glu Gly Glu Asp	Leu His Phe Pro Ala	
200	205	210
Asn Glu Lys Lys Gly Ile Glu Gln Asn	Glu Gln Trp Val Val Pro	
215	220	225
Gln Val Lys Val Glu Lys Thr Arg His	Ala Arg Gln Ala Ser Glu	
230	235	240
Glu Glu Leu Pro Ile Asn Asp Tyr Thr	Glu Asn Gly Ile Glu Phe	
245	250	255
Asp Pro Met Leu Asp Glu Arg Gly Tyr	Cys Cys Ile Tyr Cys Arg	
260	265	270
Arg Gly Asn Arg Tyr Cys Arg Arg Val	Cys Glu Pro Leu Leu Gly	
275	280	285
Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln	Gly Gly Arg Val Ile Cys	
290	295	300
Arg Val Ile Met Pro Cys Asn Trp Trp	Val Ala Arg Met Leu Gly	
305	310	315
Arg Val		

<210> 323
<211> 1174
<212> DNA
<213> Homo sapiens

<400> 323
gcggaactgg ctccggctgg cacctgagga gcggcgtgac cccgagggcc 50

cagggagctg cccggctggc cttaggcaggc agccgcacca tggccagcac 100
ggccgtgcag cttctggct tcctgctcg cttcctggc atggtggca 150
cgttgatcac caccatcctg ccgcactggc ggaggacagc gcacgtggc 200
accaacatcc tcacggccgt gtcctacctg aaagggtct ggatggagt 250
tgtgtggcac agcacaggca tctaccatgt ccagatctac cgatccctgc 300
tggcgctgcc ccaagacctc caggctgccc gcgcctcat ggtcatctcc 350
tgccctgctct cgggcatacg ctgcgcctgc gccgtcatcg ggatgaagt 400
cacgcgctgc gccaaggga cacccgc aa gaccacctt gccatcctcg 450
gcggcaccct cttcatcctg gccggcctcc tgtgcattgt ggccgtctcc 500
tggaccacca acgacgttgt gcagaacttc tacaacccgc tgctgcccag 550
cgcatgaag tttgagattt gccaggccct gtacctggc ttcatctcct 600
cgtccctctc gtcatttgtt ggcaccctgc tttgcctgtc ctgccaggac 650
gaggcaccct acaggcccta ccaggccccg cccaggggca ccacgaccac 700
tgcaaacacc gcacctgcct accagccacc agctgcctac aaagacaatc 750
gggccccctc agtgcacctcg gccacgcaca gcgggtacag gctgaacgac 800
tacgtgtgag tccccacagc ctgcttctcc cctggctgc tgtggctgg 850
gtccccggcg ggactgtcaa tggaggcagg gttccagca caaagttac 900
ttctggcaa ttttgtatc caaggaaata atgtgaatgc gagaaatgt 950
cttagagca cagggacaga gggggaaata agaggaggag aaagctct 1000
ataccaaaga ctgaaaaaaaaaa aaatcctgtc tgaaaaatgtttaatata 1050
atatttatgt ggggtatgg ataacaagtt taatataaag tgacttggga 1100
gtttggtcag tggggtttgtt ttgtgatcca ggaataaacc ttgcggatgt 1150
ggctgtttat gaaaaaaaaaaa aaaa 1174

<210> 324

<211> 239

<212> PRT

<213> Homo sapiens

<400> 324

Met	Ala	Ser	Thr	Ala	Val	Gln	Leu	Leu	Gly	Phe	Leu	Leu	Ser	Phe
1														15

Leu Gly Met Val Gly Thr Leu Ile Thr Thr Ile Leu Pro His Trp

	20	25	30
Arg Arg Thr Ala His Val Gly Thr Asn Ile Leu Thr Ala Val Ser			
	35	40	45
Tyr Leu Lys Gly Leu Trp Met Glu Cys Val Trp His Ser Thr Gly			
	50	55	60
Ile Tyr Gln Cys Gln Ile Tyr Arg Ser Leu Leu Ala Leu Pro Gln			
	65	70	75
Asp Leu Gln Ala Ala Arg Ala Leu Met Val Ile Ser Cys Leu Leu			
	80	85	90
Ser Gly Ile Ala Cys Ala Cys Ala Val Ile Gly Met Lys Cys Thr			
	95	100	105
Arg Cys Ala Lys Gly Thr Pro Ala Lys Thr Thr Phe Ala Ile Leu			
	110	115	120
Gly Gly Thr Leu Phe Ile Leu Ala Gly Leu Leu Cys Met Val Ala			
	125	130	135
Val Ser Trp Thr Thr Asn Asp Val Val Gln Asn Phe Tyr Asn Pro			
	140	145	150
Leu Leu Pro Ser Gly Met Lys Phe Glu Ile Gly Gln Ala Leu Tyr			
	155	160	165
Leu Gly Phe Ile Ser Ser Leu Ser Leu Ile Gly Gly Thr Leu			
	170	175	180
Leu Cys Leu Ser Cys Gln Asp Glu Ala Pro Tyr Arg Pro Tyr Gln			
	185	190	195
Ala Pro Pro Arg Ala Thr Thr Thr Ala Asn Thr Ala Pro Ala			
	200	205	210
Tyr Gln Pro Pro Ala Ala Tyr Lys Asp Asn Arg Ala Pro Ser Val			
	215	220	225
Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val			
	230	235	

<210> 325
<211> 2121
<212> DNA
<213> Homo sapiens

<400> 325
gagctccct caggagcgcg tttagttcac accttcggca gcaggaggc 50
ggcagcttct cgccaggcggc agggcgggcg gccaggatca tgtccaccac 100
cacatgccaa gtgggtggcgt tcctcctgtc catcctgggg ctggccggct 150
gcatcgcggc caccggatg gacatgtgga gcacccagga cctgtacgac 200

aaccccgta cctccgttt ccagtacgaa gggctctgga ggagctgcgt 250
gaggcagagt tcaggctca ccgaatgcag gccctatttc accatcctgg 300
gacttccagc catgctgcag gcagtgcgag ccctgatgat cgtaggcatc 350
gtcctgggtg ccattggct cctggtatcc atcttgccc tgaaaatgcat 400
ccgcattggc agcatggagg actctgccaa agccaacatg acactgacct 450
ccgggatcat gttcattgtc tcaggtctt gtgcaattgc tggagtgtct 500
gtgttgcca acatgctggt gactaacttc tggatgtcca cagctaacat 550
gtacaccggc atgggtggga tgggtcagac tggtcagacc aggtacacat 600
ttggtgccgc tctgttcgtg ggctgggtcg ctggaggcct cacactaatt 650
gggggtgtga ttagtgtcat cgccctgccgg ggcctggcac cagaagaaac 700
caactacaaa gccgttctt atcatgcctc aggccacagt gttgcctaca 750
agcctggagg cttcaaggcc agcactggct ttgggtccaa cacaaaaac 800
aagaagatat acgatggagg tgcccgaca gaggacgagg tacaatctta 850
tccttccaag cacgactatg tgtaatgctc taagacctct cagcacggc 900
ggaagaaact cccggagagc tcacccaaaa aacaaggaga tccccatctag 950
atttcttctt gctttgact cacagctgga agttaaaaa gcctcgattt 1000
catctttgga gaggccaaat ggtcttagcc tcaagtcctcg tctctaaata 1050
ttccaccata aaacagctga gttattttatg aatttagaggc tatagctcac 1100
atttcaatc ctctatttct tttttaaat ataactttct actctgatga 1150
gagaatgtgg tttaatctc tctctcacat tttgatgatt tagacagact 1200
ccccctcttc ctccctagta ataaacccat tgatgatcta tttccagct 1250
tatccccaaag aaaacttttg aaaggaaaga gtagacccaa agatgttatt 1300
ttctgctgtt tgaattttgt ctccccaccc ccaacttggc tagtaataaa 1350
cacttactga agaagaagca ataagagaaa gatattgta atctctccag 1400
cccatgatct cggtttctt acactgtgat cttaaaagtt accaaaccaa 1450
agtcattttc agttttaggc aaccaaacct ttctactgct gttgacatct 1500
tcttattaca gcaacaccat tcttaggagtt tcctgagctc tccactggag 1550
tcctctttct gtcgcgggtc agaaattgtc cctagatgaa tgagaaaatt 1600

attttttta atttaagtcc taaatatagt taaaataaat aatgttttag 1650
taaaatgata cactatctc gtgaaatagc ctcaccccta catgtggata 1700
gaaggaaatg aaaaaataat tgcttgaca ttgtctatat ggtacttgt 1750
aaagtcatgc ttaagtacaa attccatgaa aagctcacac ctgtaatcct 1800
agcactttgg gaggctgagg aggaaggatc acttgagccc agaagttcga 1850
gactagcctg ggcaacatgg agaagccctg tctctacaaa atacagagag 1900
aaaaaatcag ccagtcatgg tggcatacac ctgttagtccc agcattccgg 1950
gaggctgagg tgggaggatc acttgagccc agggaggttggggctgcagt 2000
gagccatgat cacaccactg cactccagcc aggtgacata gcgagatcct 2050
gtctaaaaaaaaataaaata aataatggaa cacagcaagt cctaggaagt 2100
aggtaaaac taattcttta a 2121

<210> 326

<211> 261

<212> PRT

<213> Homo sapiens

<400> 326

Met	Ser	Thr	Thr	Cys	Gln	Val	Val	Ala	Phe	Leu	Leu	Ser	Ile
1													15

Leu	Gly	Leu	Ala	Gly	Cys	Ile	Ala	Ala	Thr	Gly	Met	Asp	Met	Trp
						20			25					30

Ser	Thr	Gln	Asp	Leu	Tyr	Asp	Asn	Pro	Val	Thr	Ser	Val	Phe	Gln
					35				40					45

Tyr	Glu	Gly	Leu	Trp	Arg	Ser	Cys	Val	Arg	Gln	Ser	Ser	Gly	Phe
					50				55					60

Thr	Glu	Cys	Arg	Pro	Tyr	Phe	Thr	Ile	Leu	Gly	Leu	Pro	Ala	Met
					65				70					75

Leu	Gln	Ala	Val	Arg	Ala	Leu	Met	Ile	Val	Gly	Ile	Val	Leu	Gly
					80				85					90

Ala	Ile	Gly	Leu	Leu	Val	Ser	Ile	Phe	Ala	Leu	Lys	Cys	Ile	Arg
									95					105

Ile	Gly	Ser	Met	Glu	Asp	Ser	Ala	Lys	Ala	Asn	Met	Thr	Leu	Thr
									110				115	120

Ser	Gly	Ile	Met	Phe	Ile	Val	Ser	Gly	Leu	Cys	Ala	Ile	Ala	Gly
									125				130	135

Val	Ser	Val	Phe	Ala	Asn	Met	Leu	Val	Thr	Asn	Phe	Trp	Met	Ser
									140				145	150

Thr Ala Asn Met Tyr Thr Gly Met Gly Gly Met Val Gln Thr Val
155 160 165
Gln Thr Arg Tyr Thr Phe Gly Ala Ala Leu Phe Val Gly Trp Val
170 175 180
Ala Gly Gly Leu Thr Leu Ile Gly Gly Val Met Met Cys Ile Ala
185 190 195
Cys Arg Gly Leu Ala Pro Glu Glu Thr Asn Tyr Lys Ala Val Ser
200 205 210
Tyr His Ala Ser Gly His Ser Val Ala Tyr Lys Pro Gly Gly Phe
215 220 225
Lys Ala Ser Thr Gly Phe Gly Ser Asn Thr Lys Asn Lys Lys Ile
230 235 240
Tyr Asp Gly Gly Ala Arg Thr Glu Asp Glu Val Gln Ser Tyr Pro
245 250 255
Ser Lys His Asp Tyr Val
260

<210> 327
<211> 2010
<212> DNA
<213> Homo sapiens

<400> 327
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gtacgcgttc cggagtcacat ctggctaaaaa ctcatccacaggataatgg 100
caacccatgc ctttagaaatc gctggctgtt ttcttggtgg tgttggaaatg 150
gtgggcacag tggctgtcac tgtcatgcct cagtggagag tgtcggcctt 200
cattgaaaac aacatcgtagg ttttgaaaaa cttctggaa ggactgtgga 250
tgaattgcgt gaggcaggct aacatcgatggatc tgcaatgcggaa aatctatgtat 300
tccctgctgg ctctttctcc ggacctacag gcagccacagg gactgatgtg 350
tgctgcttcc gtgatgtcct tcttggcttt catgatggcc atccttggca 400
tgaaatgcac caggtgcacgg ggggacaatg agaagggtgaa ggctcacatt 450
ctgctgacgg ctggaaatcat cttcatcatc acgggcatgg tggtgctcat 500
ccctgtgagc tgggttgcca atgccccatcat cagagatttc tataactcaa 550
tagtgaatgt tgcccaaaaaa cgtgagcttg gagaagctct ctacttagga 600
tggaccacgg cactggtgct gattgttgaa ggagctctgt tctgctgcgt 650

ttttgttgc aacgaaaaga gcagtagcta cagatactcg atacttccc 700
atcgacaac ccaaaaaagt tatcacaccg gaaagáagtc accgagcgtc 750
tactccagaa gtcagtatgt gtatgtgt atgttttt aacttacta 800
taaagccatg caaatgacaa aaatctatat tacttctca aatggaccc 850
caaagaaaact ttgatttact gttcttaact gcctaatttt aattacagga 900
actgtgcata agctatTTT gattctataa gctatTCAG cagaatgaga 950
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taagggtgtt caagcatcta ctcttttat cattacttc aaaatgacat 1050
tgctaaagac tgcattattt tactactgta atttctccac gacatagcat 1100
tatgtacata gatgagtgt acaTTTATCTCACATAGA gacatgctt 1150
tatggTTTA ttAAAATGA aatGCCAGTC cattacactg aATAAAATAGA 1200
actcaactat tgctttcag ggAAATCATG gatAGGGTTG aAGAAGGTTA 1250
ctattaATTG ttAAAAACCA gcttagggat taatgcctc catttataat 1300
gaagattaaa atgaaggcTT taatcagcat tgtaaaggaa attgaatggc 1350
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gagtacagac ttgaggttt catcaatata aataAAAGAG cagaaaaata 1700
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atTTTGTTC tgtgaaaaat aaatttcctt ctgtaccat ttctgttttag 1850
tttactaaa atctgtAAAT actgtatTTT tctgtttatt ccaaatttga 1900
tgaAAACTGAC aatccaattt gaaagTTGT gtcgacgtct gtctagctt 1950
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ttttctaatt 2010

<211> 225
<212> PRT
<213> Homo sapiens

<400> 328

Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly		
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Val Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp		
20	25	30
Arg Val Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn		
35	40	45
Phe Trp Glu Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile		
50	55	60
Arg Met Gln Cys Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro		
65	70	75
Asp Leu Gln Ala Ala Arg Gly Leu Met Cys Ala Ala Ser Val Met		
80	85	90
Ser Phe Leu Ala Phe Met Met Ala Ile Leu Gly Met Lys Cys Thr		
95	100	105
Arg Cys Thr Gly Asp Asn Glu Lys Val Lys Ala His Ile Leu Leu		
110	115	120
Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly Met Val Val Leu Ile		
125	130	135
Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg Asp Phe Tyr Asn		
140	145	150
Ser Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly Glu Ala Leu		
155	160	165
Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile Val Gly Gly Ala		
170	175	180
Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser Ser Ser Tyr		
185	190	195
Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser Tyr His		
200	205	210
Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr Val		
215	220	225

<210> 329
<211> 1315
<212> DNA
<213> Homo sapiens

<400> 329
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gaccgc tttc atcgcaaca gcatcgtggt gcccaggtg gtgtgggagg 150
gcctgtggat gtcctgcgtg gtgcagagca cccgcagat gcagtgc aag 200
gtgtacgact cactgctggc gtcgccacag gacgcagg ctgcacgtgc 250
cctctgtgtc atcgccctcc ttgtggccct gttcggcttg ctggtctacc 300
ttgctgggc caagtgtacc acctgtgtgg aggagaaggta ttccaaggcc 350
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gctaatacccc gtgtgtggc cgccgcatgc catcatccgg gacttctata 450
accccccgtt ggctgaggcc caaaagcggg agctgggggc ctccctctac 500
ttgggctggg cgccctcagg cctttgttg ctgggtgggg gttgtgtg 550
ctgcacttgc ccctcggggg ggtcccaggcc cccagccat tacatggccc 600
gctactcaac atctgcccct gccatctctc gggggccctc tgagtaccct 650
accaagaatt acgtctgacg tggaggggaa tgggggctcc gctggcgcta 700
gagccatcca gaagtggcag tgcccaacag ctttggatg gttcgtacc 750
ttttgttct gcctcctgct atttttctt tgactgagga tatttaaat 800
tcatttggaaa actgagccaa ggtgttgact cagactctca cttaggctct 850
gctgtttctc acccttggat gatggagccaa aagaggggat gctttgagat 900
tctggatctt gacatgccc a tcttagaagc cagtcaagct atgaaactaa 950
tgcggaggct gttgtgtg ctggcttgc aacaagacag actgtcccc 1000
agagttcctg ctgctgctgg gggctggct tccctagatg tcactggaca 1050
gctgcccccc atcctactca ggtctctgg a gtcctctct tcacccctgg 1100
aaaaacaaat catctgttcaa caaaggactg cccaccccg gaaacttctga 1150
cctctgtttc ctccgtcctg ataagacgtc cacccccccag gcccaggcc 1200
cagctatgta gacccccc cccacccca acactgcacc cttctgccc 1250
gccccccctcg tctcacccccc ttacactca catttttataa aaataaagca 1300
tgttttggta gtgca 1315

<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

Met Ala Ser Ala Gly Met Gln Ile Leu Gly Val Val Leu Thr Leu
1 5 10 15

Leu Gly Trp Val Asn Gly Leu Val Ser Cys Ala Leu Pro Met Trp
20 25 30

Lys Val Thr Ala Phe Ile Gly Asn Ser Ile Val Val Ala Gln Val
35 40 45

Val Trp Glu Gly Leu Trp Met Ser Cys Val Val Gln Ser Thr Gly
50 55 60

Gln Met Gln Cys Lys Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln
65 70 75

Asp Leu Gln Ala Ala Arg Ala Leu Cys Val Ile Ala Leu Leu Val
80 85 90

Ala Leu Phe Gly Leu Leu Val Tyr Leu Ala Gly Ala Lys Cys Thr
95 100 105

Thr Cys Val Glu Glu Lys Asp Ser Lys Ala Arg Leu Val Leu Thr
110 115 120

Ser Gly Ile Val Phe Val Ile Ser Gly Val Leu Thr Leu Ile Pro
125 130 135

Val Cys Trp Thr Ala His Ala Ile Ile Arg Asp Phe Tyr Asn Pro
140 145 150

Leu Val Ala Glu Ala Gln Lys Arg Glu Leu Gly Ala Ser Leu Tyr
155 160 165

Leu Gly Trp Ala Ala Ser Gly Leu Leu Leu Gly Gly Gly Leu
170 175 180

Leu Cys Cys Thr Cys Pro Ser Gly Gly Ser Gln Gly Pro Ser His
185 190 195

Tyr Met Ala Arg Tyr Ser Thr Ser Ala Pro Ala Ile Ser Arg Gly
200 205 210

Pro Ser Glu Tyr Pro Thr Lys Asn Tyr Val
215 220

<210> 331

<211> 1160

<212> DNA

<213> Homo sapiens

<400> 331

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gtaaaggcaa tggcattta tcccttgcaaa attgctggc tggttcttgg 150
gttccttggc atgggtggga ctcttgccac aacccttctg cctcagtgg 200
ggagtatcag cttttggc cagcaacatt attgtcttg agaggctctg 250
ggaagggctc tggatgaatt gcatccgaca agccagggtc cggttgcaat 300
gcaagttcta tagtccttg ttggctctcc cgccctgcct ggaaacagcc 350
cggccctca tgtgtgtggc tggtgctctc tccttgatcg ccctgcttat 400
tggcatctgt ggcataatggc aggtccagtg cacaggctct aacgagaggg 450
ccaaagcata cttctggaa acttcaggag tcctttcat cctgacgggt 500
atcttcgttc tgattccggc gagctggaca gccaatataa tcatcagaga 550
tttctacaac ccagccatcc acataggtca gaaacgagag ctgggagcag 600
cactttcct tggctggca agcgctgctg tcctttcat tggaggggt 650
ctgctttgtg gatttgctg ctgcaacaga aagaagcaag ggtacagata 700
tccagtgcct ggctaccgtg tgccacacac agataagcga agaaatacga 750
caatgcttag taagacctcc accagttatg tctaattgcct cttttggct 800
ccaagtatgg actatggtca atgtttttta taaagtctg ctagaaactg 850
taagtatgtg aggccaggaga acttgctta tgtcttagatt tacattgata 900
cgaaagttc aatttggcac tggggtagg aatgaaaatg acttacttgg 950
acattctgac ttcaggtgtt aaaaatgcat tgactattgt tggacccaat 1000
cgctgctcca atttcatat tctaaattca agtataacca taatcattag 1050
caagtgtaca atgatggact acttattact ttttgaccat catgtattat 1100
ctgataagaa tctaaagttg aaattgatata tctataacaa taaaacatata 1150
acctattctta 1160

<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

Met	Asn	Cys	Ile	Arg	Gln	Ala	Arg	Val	Arg	Leu	Gln	Cys	Lys	Phe
1														15

Tyr	Ser	Ser	Leu	Leu	Ala	Leu	Pro	Pro	Ala	Leu	Glu	Thr	Ala	Arg
														30

Ala Leu Met Cys Val Ala Val Ala Leu Ser Leu Ile Ala Leu Leu

35	40	45
Ile Gly Ile Cys Gly Met Lys Gln Val Gln Cys Thr Gly Ser Asn		
50	55	60
Glu Arg Ala Lys Ala Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe		
65	70	75
Ile Leu Thr Gly Ile Phe Val Leu Ile Pro Val Ser Trp Thr Ala		
80	85	90
Asn Ile Ile Ile Arg Asp Phe Tyr Asn Pro Ala Ile His Ile Gly		
95	100	105
Gln Lys Arg Glu Leu Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser		
110	115	120
Ala Ala Val Leu Phe Ile Gly Gly Leu Leu Cys Gly Phe Cys		
125	130	135
Cys Cys Asn Arg Lys Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly		
140	145	150
Tyr Arg Val Pro His Thr Asp Lys Arg Arg Asn Thr Thr Met Leu		
155	160	165
Ser Lys Thr Ser Thr Ser Tyr Val		
170		

<210> 333
 <211> 535
 <212> DNA
 <213> Homo sapiens

<400> 333
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 ctcagaagct gctagtctgt ctccaaaaaa agtggactgc agcatttaca 150
 agaagtatcc agtggtgcc atccccgtcc ccatcacata cctaccagg 200
 tgtggttctg actacatcac ctatggaaat gaatgtcaat tgtgtaccga 250
 gagcttgaaa agtaatggaa gagttcagtt tcttcacgat ggaagttgct 300
 aaattctcca tggacataga gagaaaggaa tgatattctc atcatcatct 350
 tcacatccc aggctctgac ttagtttctt tcaagtttac tgatgttctg 400
 ggtgggggac agagccagat tcagagtaat cttgactgaa tggagaaagt 450
 ttctgtgcta cccctacaaa cccatgcctc actgacagac cagcatttt 500
 ttttaaacac gtcaataaaa aaataatctc ccaga 535

<210> 334
<211> 85
<212> PRT
<213> Homo sapiens

<400> 334

Met	Lys	Ile	Thr	Gly	Gly	Leu	Leu	Leu	Cys	Thr	Val	Val	Tyr
1				5				10					15

Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val

	20					25							30
--	----	--	--	--	--	----	--	--	--	--	--	--	----

Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys

	35				40								45
--	----	--	--	--	----	--	--	--	--	--	--	--	----

Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr

	50				55								60
--	----	--	--	--	----	--	--	--	--	--	--	--	----

Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly

	65				70								75
--	----	--	--	--	----	--	--	--	--	--	--	--	----

Arg Val Gln Phe Leu His Asp Gly Ser Cys

	80				85								
--	----	--	--	--	----	--	--	--	--	--	--	--	--

<210> 335
<211> 742
<212> DNA
<213> Homo sapiens

<400> 335

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tggccctgac cgggctggcg ctgctcctgc tccttgctg gggcccagg 150
ggcataagtg gaaataaaact caagctgatg cttaaaaaac gagaagcacc 200
tgttccaact aagactaaag tggccgttga tgagaataaa gccaaagaat 250
tccttggcag cctgaagcgc cagaagcggc agctgtggga ccggactcgg 300
cccgagggtgc agcagtggta ccagcagttt ctctacatgg gctttgatga 350
agcgaatattt gaagatgaca tcacctattt gcttaacaga gatcgaaatg 400
gacatgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450
gcaattggtc cccggagccc ctacggcttt aggcatggag ccagcgtcaa 500
ctacgatgac tactaaccat gacttgccac acgctgtaca agaagcaaat 550
agcgattctc ttcatgtatc tcctaattgcc ttacactact tggttctga 600
tttgctctat ttcatgtatc tcctaattgcc ttacactact tggttctga 650
gaagagttaa aacaacacat gtaaatgcct tttgatattt catggaaatg 700

cctctcattt aaaaatagaa ataaaggatt ttgttaaaaa ga 742

<210> 336

<211> 148

<212> PRT

<213> Homo sapiens

<400> 336

Met Ala Ala Ser Pro Ala Arg Pro Ala Val Leu Ala Leu Thr Gly
1 5 10 15

Leu Ala Leu Leu Leu Leu Cys Trp Gly Pro Gly Gly Ile Ser
20 25 30

Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val
35 40 45

Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu
50 55 60

Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg
65 70 75

Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met
80 85 90

Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu
95 100 105

Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln
110 115 120

Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr
125 130 135

Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr
140 145

<210> 337

<211> 1310

<212> DNA

<213> Homo sapiens

<400> 337

cggctcgagc ccgccccgaa gtgcccggagg ggccgcgatg gagctgggg 50

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tgaagggtg ggtgatgagg tgaccgtcct tttctcggtg cttgcctgcc 150

ttctggtgct ggccttgcc tgggtctcaa cgcacaccgc tgagggcggg 200

gacccactgc cccagccgtc agggacccca acgccatccc agcccagcgc 250

agccatggca gctaccgaca gcatgagagg ggaggccca gggcagaga 300

cccccagcct gagacacaga ggtcaagctg cacagccaga gcccagcacg 350
gggttcacag caacaccgccc agccccggac tccccgcagg agccccctcg 400
gctacggctg aaattcctca atgattcaga gcaggtggcc agggcctggc 450
cccacgacac cattggctcc ttgaaaagga cccagttcc cggccgggaa 500
cagcaggtgc gactcatcta ccaagggcag ctgctaggcg acgacaccca 550
gaccctggc agccttcacc tccctcccaa ctgcgttctc cactgccacg 600
tgtccacgag agtcggtccc ccaaattcccc cctgcccggcc ggggtccgag 650
cccgccccct ccgggctgga aatcggcagc ctgctgctgc ccctgctgct 700
cctgctgttg ctgctgctct ggtactgcca gatccagtac cgcccttct 750
ttccccctgac cgccactctg ggccctggccg gcttcaccct gtcctcagt 800
ctcctggcct ttgccatgta ccgccccgtag tgcctccgag ggccgttggc 850
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ctgcctgccc aggcccgcct ctccggcctg cctcttccgg ctgcctgga 950
gcccagccct gcccggcaga ggactcccg gactggcgga ggccccgccc 1000
tgcgaccgccc ggggctcgaa gcccacccccc ggggctgctg aacctcagcc 1050
cgcaactggaa gtgggctcct cggggctcgaa catctgctgt cgctgcctcg 1100
gccccgggca gagccgggccc gccccgggggg cccgtcttag tggtctgccc 1150
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acgccaggtc ggtgggaggc tggtaaggg gagcggggag gggcagagga 1250
gttccccggaa acccgtgcag attaaagtaa ctgtgaagtt taaaaaaaaa 1300
aaaaaaaaaa 1310

<210> 338
<211> 246
<212> PRT
<213> Homo sapiens

<400> 338
Met Thr Leu Ile Glu Gly Val Gly Asp Glu Val Thr Val Leu Phe
1 5 10 15
Ser Val Leu Ala Cys Leu Leu Val Leu Ala Leu Ala Trp Val Ser
20 25 30
Thr His Thr Ala Glu Gly Gly Asp Pro Leu Pro Gln Pro Ser Gly
35 40 45

Thr	Pro	Thr	Pro	Ser	Gln	Pro	Ser	Ala	Ala	Met	Ala	Ala	Thr	Asp
					50					55			60	
Ser	Met	Arg	Gly	Glu	Ala	Pro	Gly	Ala	Glu	Thr	Pro	Ser	Leu	Arg
					65				70			75		
His	Arg	Gly	Gln	Ala	Ala	Gln	Pro	Glu	Pro	Ser	Thr	Gly	Phe	Thr
					80				85			90		
Ala	Thr	Pro	Pro	Ala	Pro	Asp	Ser	Pro	Gln	Glu	Pro	Leu	Val	Leu
					95				100			105		
Arg	Leu	Lys	Phe	Leu	Asn	Asp	Ser	Glu	Gln	Val	Ala	Arg	Ala	Trp
					110				115			120		
Pro	His	Asp	Thr	Ile	Gly	Ser	Leu	Lys	Arg	Thr	Gln	Phe	Pro	Gly
					125				130			135		
Arg	Glu	Gln	Gln	Val	Arg	Leu	Ile	Tyr	Gln	Gly	Gln	Leu	Leu	Gly
					140				145			150		
Asp	Asp	Thr	Gln	Thr	Leu	Gly	Ser	Leu	His	Leu	Pro	Pro	Asn	Cys
					155				160			165		
Val	Leu	His	Cys	His	Val	Ser	Thr	Arg	Val	Gly	Pro	Pro	Asn	Pro
					170				175			180		
Pro	Cys	Pro	Pro	Gly	Ser	Glu	Pro	Gly	Pro	Ser	Gly	Leu	Glu	Ile
					185				190			195		
Gly	Ser	Leu	Leu	Leu	Pro	Leu								
					200				205			210		
Trp	Tyr	Cys	Gln	Ile	Gln	Tyr	Arg	Pro	Phe	Phe	Pro	Leu	Thr	Ala
					215				220			225		
Thr	Leu	Gly	Leu	Ala	Gly	Phe	Thr	Leu	Leu	Leu	Ser	Leu	Leu	Ala
					230				235			240		
Phe	Ala	Met	Tyr	Arg	Pro									
					245									

<210> 339

<211> 849

<212> DNA

<213> Homo sapiens

<400> 339

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caagacccta agaaccatca gccctcagct gcacccctc ccctccaagg 150

atgacaaagg cgctactcat ctatggtc agcagttc ttgccctaaa 200

tcaggccagc ctcatacgatc gctgtgactt ggcccagggtc ctgcagctgg 250

aggacttgg a tggttttag ggttactccc tgagtgactg gctgtgcctg 300
gcttttgtgg aaagcaagtt caacatatca aagataaatg aaaatgcgga 350
t gaaagcttt gactatggcc tcttccagat caacagccac tactggtgca 400
acgattataa gagttactcg gaaaacctt gccacgtaga ctgtcaagat 450
ctgctgaatc ccaaccttct tcgaggcatc cactgcgcaa aaaggattgt 500
gtccggagca cgggggatga acaactgggt agaatggagg ttgcactgtt 550
caggccggcc actctcctac tggctgacag gatgccgcct gagatgaaac 600
agggtgcggg tgcaccgtgg agtcattcca agactcctgt cctcactca 650
ggattcttca tttcttcttc ctactgcctc cacttcatgt tattttcttc 700
cctcccccatt tacaactaaa actgaccaga gccccagaa taaatggttt 750
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<210> 340

<211> 148

<212> PRT

<213> Homo sapiens

<400> 340

Met Thr Lys Ala Leu Leu Ile Tyr Leu Val Ser Ser Phe Leu Ala
1 5 10 15

Leu Asn Gln Ala Ser Leu Ile Ser Arg Cys Asp Leu Ala Gln Val
20 25 30

Leu Gln Leu Glu Asp Leu Asp Gly Phe Glu Gly Tyr Ser Leu Ser
35 40 45

Asp Trp Leu Cys Leu Ala Phe Val Glu Ser Lys Phe Asn Ile Ser
50 55 60

Lys Ile Asn Glu Asn Ala Asp Gly Ser Phe Asp Tyr Gly Leu Phe
65 70 75

Gln Ile Asn Ser His Tyr Trp Cys Asn Asp Tyr Lys Ser Tyr Ser
80 85 90

Glu Asn Leu Cys His Val Asp Cys Gln Asp Leu Leu Asn Pro Asn
95 100 105

Leu Leu Ala Gly Ile His Cys Ala Lys Arg Ile Val Ser Gly Ala
110 115 120

Arg Gly Met Asn Asn Trp Val Glu Trp Arg Leu His Cys Ser Gly
125 130 135

Arg Pro Leu Ser Tyr Trp Leu Thr Gly Cys Arg Leu Arg
140 145

<210> 341

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 341

ccctccaagg atgacaaaagg cgc 23

<210> 342

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 342

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<210> 343

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 343

atctcaggcg gcatcctgtc agcc 24

<210> 344

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 344

gtggatgcct gcaagaaggt tggg 24

<210> 345

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 345

agctttcttg ccctaaatca gcccagcctc atcagtcgct gtgac 45

<210> 346

<211> 2575

<212> DNA

<213> Homo sapiens

<400> 346

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actgagaacc caccagctca tcccagacac ctcatagcaa cctatttata 100

caaaggggga aagaaacacc tgagcagaat ggaatcatta ttttttccc 150

aaggagaaaa ccggggtaaa gggagggaaag caattcaatt tgaagtccct 200

gtgaatgggc tttcagaagg caattaaaga aatccactca gagaggactt 250

gggggtgaaac ttgggtcctg tggtttctg attgttaagtg gaagcaggc 300

ttgcacacgc ttttggcaaa tgtcaggacc aggttaagtg actggcagaa 350

aaacttccag gtggacaacaag caacccatgt tctgtcgcaa gcttgaagga 400

gcctggagcg ggagaaagct aacttgaaca tgacctgttgcatttggca 450

gttctagcaa catgtccta aggaagcgat acaggcacag accatgcaga 500

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<210> 347
<211> 639

<212> PRT

<213> Homo sapiens

<400> 347

Met Leu Leu Arg Lys Arg Tyr Arg His Arg Pro Cys Arg Leu Gln
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Phe Leu Leu Leu Leu Met Leu Gly Cys Val Leu Met Met Val
20 25 30

Ala Met Leu His Pro Pro His His Thr Leu His Gln Thr Val Thr
35 40 45

Ala Gln Ala Ser Lys His Ser Pro Glu Ala Arg Tyr Arg Leu Asp
50 55 60

Phe Gly Glu Ser Gln Asp Trp Val Leu Glu Ala Glu Asp Glu Gly
65 70 75

Glu Glu Tyr Ser Pro Leu Glu Gly Leu Pro Pro Phe Ile Ser Leu
80 85 90

Arg Glu Asp Gln Leu Leu Val Ala Val Ala Leu Pro Gln Ala Arg
95 100 105

Arg Asn Gln Ser Gln Gly Arg Arg Gly Ser Tyr Arg Leu Ile
110 115 120

Lys Gln Pro Arg Arg Gln Asp Lys Glu Ala Pro Lys Arg Asp Trp
125 130 135

Gly Ala Asp Glu Asp Gly Glu Val Ser Glu Glu Glu Leu Thr
140 145 150

Pro Phe Ser Leu Asp Pro Arg Gly Leu Gln Glu Ala Leu Ser Ala
155 160 165

Arg Ile Pro Leu Gln Arg Ala Leu Pro Glu Val Arg His Pro Leu
170 175 180

Cys Leu Gln Gln His Pro Gln Asp Ser Leu Pro Thr Ala Ser Val
185 190 195

Ile Leu Cys Phe His Asp Glu Ala Trp Ser Thr Leu Leu Arg Thr
200 205 210

Val His Ser Ile Leu Asp Thr Val Pro Arg Ala Phe Leu Lys Glu
215 220 225

Ile Ile Leu Val Asp Asp Leu Ser Gln Gln Gly Gln Leu Lys Ser
230 235 240

Ala Leu Ser Glu Tyr Val Ala Arg Leu Glu Gly Val Lys Leu Leu
245 250 255

Arg Ser Asn Lys Arg Leu Gly Ala Ile Arg Ala Arg Met Leu Gly
260 265 270

Ala Thr Arg Ala Thr Gly Asp Val Leu Val Phe Met Asp Ala His
275 280 285

Cys Glu Cys His Pro Gly Trp Leu Glu Pro Leu Leu Ser Arg Ile
290 295 300

Ala Gly Asp Arg Ser Arg Val Val Ser Pro Val Ile Asp Val Ile
305 310 315

Asp Trp Lys Thr Phe Gln Tyr Tyr Pro Ser Lys Asp Leu Gln Arg
320 325 330

Gly Val Leu Asp Trp Lys Leu Asp Phe His Trp Glu Pro Leu Pro
335 340 345

Glu His Val Arg Lys Ala Leu Gln Ser Pro Ile Ser Pro Ile Arg
350 355 360

Ser Pro Val Val Pro Gly Glu Val Val Ala Met Asp Arg His Tyr
365 370 375

Phe Gln Asn Thr Gly Ala Tyr Asp Ser Leu Met Ser Leu Arg Gly
380 385 390

Gly Glu Asn Leu Glu Leu Ser Phe Lys Ala Trp Leu Cys Gly Gly
395 400 405

Ser Val Glu Ile Leu Pro Cys Ser Arg Val Gly His Ile Tyr Gln
410 415 420

Asn Gln Asp Ser His Ser Pro Leu Asp Gln Glu Ala Thr Leu Arg
425 430 435

Asn Arg Val Arg Ile Ala Glu Thr Trp Leu Gly Ser Phe Lys Glu
440 445 450

Thr Phe Tyr Lys His Ser Pro Glu Ala Phe Ser Leu Ser Lys Ala
455 460 465

Glu Lys Pro Asp Cys Met Glu Arg Leu Gln Leu Gln Arg Arg Leu
470 475 480

Gly Cys Arg Thr Phe His Trp Phe Leu Ala Asn Val Tyr Pro Glu
485 490 495

Leu Tyr Pro Ser Glu Pro Arg Pro Ser Phe Ser Gly Lys Leu His
500 505 510

Asn Thr Gly Leu Gly Leu Cys Ala Asp Cys Gln Ala Glu Gly Asp
515 520 525

Ile Leu Gly Cys Pro Met Val Leu Ala Pro Cys Ser Asp Ser Arg
530 535 540

Gln Gln Gln Tyr Leu Gln His Thr Ser Arg Lys Glu Ile His Phe
545 550 555

Gly Ser Pro Gln His Leu Cys Phe Ala Val Arg Gln Glu Gln Val
560 565 570

Ile Leu Gln Asn Cys Thr Glu Glu Gly Leu Ala Ile His Gln Gln
575 580 585

His Trp Asp Phe Gln Glu Asn Gly Met Ile Val His Ile Leu Ser
590 595 600

Gly Lys Cys Met Glu Ala Val Val Gln Glu Asn Asn Lys Asp Leu
605 610 615

Tyr Leu Arg Pro Cys Asp Gly Lys Ala Arg Gln Gln Trp Arg Phe
620 625 630

Asp Gln Ile Asn Ala Val Asp Glu Arg
635

<210> 348
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 348
ggagagggtgg tggccatgga cag 23

<210> 349
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 349
ctgtcactgc aaggagccaa cacc 24

<210> 350
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 350
tatgtcgctg cgaggtggtg aaaacctcgaa actgttttc aaggc 45

<210> 351
<211> 2524
<212> DNA
<213> Homo sapiens

<400> 351
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tccctctctg gccactgctg ttgctgcccc tcccaccgccc tgctcagggc 150
tcttcattcct cccctcgaac cccaccagcc ccagcccgcc ccccgtgtgc 200
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<210> 352

<211> 243

<212> PRT

<213> Homo sapiens

<400> 352

Met	Arg	Pro	Gln	Gly	Pro	Ala	Ala	Ser	Pro	Gln	Arg	Leu	Arg	Gly
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Leu	Leu	Leu	Leu	Leu	Leu	Gln	Leu	Pro	Ala	Pro	Ser	Ser	Ala	
							20		25			30		

Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
 35 40 45

 Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
 50 55 60

 Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
 65 70 75

 Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
 80 85 90

 Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
 95 100 105

 Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
 110 115 120

 Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
 125 130 135

 Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg
 140 145 150

 Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu
 155 160 165

 Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln
 170 175 180

 Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser
 185 190 195

 Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp
 200 205 210

 Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp
 215 220 225

 Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu
 230 235 240

 Leu Pro Lys

<210> 353
 <211> 480
 <212> DNA
 <213> Homo sapiens

<400> 353
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cgtgcccacg ctgtggaacg agccggccga gctgccgtcg ggagaaggcc 200
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gccccccacg tcgcgccagg acccgaggac agcaccgcgc aggagcggct 300
ggaccagggc ggccgggtcgc tggggcccggtcgctatcgcg gccatcgta 350
tcgcccct gctggccacc tgctgggtgc tggcgctcggtcg 400
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gcggcgac tcggcaaaaa aaaaaaaaaa 480

<210> 354

<211> 121

<212> PRT

<213> Homo sapiens

<400> 354

Met Ala Ser Cys Leu Ala Leu Arg Met Ala Leu Leu Leu Val Ser
1 5 10 15

Gly Val Leu Ala Pro Ala Val Leu Thr Asp Asp Val Pro Gln Glu
20 25 30

Pro Val Pro Thr Leu Trp Asn Glu Pro Ala Glu Leu Pro Ser Gly
35 40 45

Glu Gly Pro Val Glu Ser Thr Ser Pro Gly Arg Glu Pro Val Asp
50 55 60

Thr Gly Pro Pro Ala Pro Thr Val Ala Pro Gly Pro Glu Asp Ser
65 70 75

Thr Ala Gln Glu Arg Leu Asp Gln Gly Gly Ser Leu Gly Pro
80 85 90

Gly Ala Ile Ala Ala Ile Val Ile Ala Ala Leu Leu Ala Thr Cys
95 100 105

Val Val Leu Ala Leu Val Val Ala Leu Arg Lys Phe Ser Ala
110 115 120

Ser

<210> 355

<211> 2134

<212> DNA

<213> Homo sapiens

<400> 355

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gtgcctgacg gcggcgctgg cccacggctg tctgcactgc cacagcaact 150
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ctgcggatg tgattaaagt ccctgatgtt tctc 2134

<210> 356

<211> 157

<212> PRT

<213> Homo sapiens

<400> 356

Met Ala Leu Leu Leu Cys Leu Val Cys Leu Thr Ala Ala Leu Ala
1 5 10 15

His Gly Cys Leu His Cys His Ser Asn Phe Ser Lys Lys Phe Ser
20 25 30

Phe Tyr Arg His His Val Asn Phe Lys Ser Trp Trp Val Gly Asp
35 40 45

Ile Pro Val Ser Gly Ala Leu Leu Thr Asp Trp Ser Asp Asp Thr
50 55 60

Met Lys Glu Leu His Leu Ala Ile Pro Ala Lys Ile Thr Arg Glu
65 70 75

Lys Leu Asp Gln Val Ala Thr Ala Val Tyr Gln Met Met Asp Gln
80 85 90

Leu Tyr Gln Gly Lys Met Tyr Phe Pro Gly Tyr Phe Pro Asn Glu
95 100 105

Leu Arg Asn Ile Phe Arg Glu Gln Val His Leu Ile Gln Asn Ala
110 115 120

Ile Ile Glu Arg His Leu Ala Pro Gly Ser Trp Gly Gly Gln

	125	130	135
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	140	145	150
Ser Pro Arg Gly Asp Leu Pro			
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<210> 357			
<211> 1536			
<212> DNA			
<213> Homo sapiens			
<400> 357			
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cagaagttaa aggctgtctc caagtccctg aactcagcag aaatagacca 1450
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caacctgcat aataaataaa aggcaatcat gttata 1536

<210> 358

<211> 273

<212> PRT

<213> Homo sapiens

<400> 358

Met	Glu	Ala	Ala	Pro	Ser	Arg	Phe	Met	Phe	Leu	Leu	Phe	Leu	Leu
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Thr	Cys	Glu	Leu	Ala	Ala	Glu	Val	Ala	Ala	Glu	Val	Glu	Lys	Ser
				20					25					30
Ser	Asp	Gly	Pro	Gly	Ala	Ala	Gln	Glu	Pro	Thr	Trp	Leu	Thr	Asp
				35				40						45
Val	Pro	Ala	Ala	Met	Glu	Phe	Ile	Ala	Ala	Thr	Glu	Val	Ala	Val
				50					55					60
Ile	Gly	Phe	Phe	Gln	Asp	Leu	Glu	Ile	Pro	Ala	Val	Pro	Ile	Leu
				65					70					75
His	Ser	Met	Val	Gln	Lys	Phe	Pro	Gly	Val	Ser	Phe	Gly	Ile	Ser
				80					85					90
Thr	Asp	Ser	Glu	Val	Leu	Thr	His	Tyr	Asn	Ile	Thr	Gly	Asn	Thr
				95					100					105
Ile	Cys	Leu	Phe	Arg	Leu	Val	Asp	Asn	Glu	Gln	Leu	Asn	Leu	Glu
				110					115					120
Asp	Glu	Asp	Ile	Glu	Ser	Ile	Asp	Ala	Thr	Lys	Leu	Ser	Arg	Phe
				125					130					135
Ile	Glu	Ile	Asn	Ser	Leu	His	Met	Val	Thr	Glu	Tyr	Asn	Pro	Val
				140					145					150
Thr	Val	Ile	Gly	Leu	Phe	Asn	Ser	Val	Ile	Gln	Ile	His	Leu	Leu
				155					160					165

Leu Ile Met Asn Lys Ala Ser Pro Glu Tyr Glu Glu Asn Met His
170 175 180

Arg Tyr Gln Lys Ala Ala Lys Leu Phe Gln Gly Lys Ile Leu Phe
185 190 195

Ile Leu Val Asp Ser Gly Met Lys Glu Asn Gly Lys Val Ile Ser
200 205 210

Phe Phe Lys Leu Lys Glu Ser Gln Leu Pro Ala Leu Ala Ile Tyr
215 220 225

Gln Thr Leu Asp Asp Glu Trp Asp Thr Leu Pro Thr Ala Glu Val
230 235 240

Ser Val Glu His Val Gln Asn Phe Cys Asp Gly Phe Leu Ser Gly
245 250 255

Lys Leu Leu Lys Glu Asn Arg Glu Ser Glu Gly Lys Thr Pro Lys
260 265 270

Val Glu Leu

<210> 359
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 359
ccagcagtgc ccatactcca tagc 24

<210> 360
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 360
tgacgagtgg gatacactgc 20

<210> 361
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 361
gctctacgga aacttctgct gtgg 24

<210> 362
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 362
attcccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363
<211> 1777
<212> DNA
<213> Homo sapiens

<400> 363
ggagagccgc ggctgggacc ggagtgggaa gcgcggcgta gaggtgccac 50
ccggcgcggg tggcggagag atcagaagcc tttccccaa gccgagccaa 100
cctcagcggg gacccgggct cagggacgcg gggcgccgg cggcactgc 150
agtggcttga cgatggcagc gtccggccga gccggggcg tgattgcagc 200
cccagacagc cggcgctggc tgtggtcggt gctggcgccg gcgcttggc 250
tcttgcacgc tggagtatca gccttggaaat tatatacgcc aaaagaaaatc 300
ttcgtggcaa atggcacaca agggaaagctg acctcaagt tcaagtctac 350
tagtacgact ggcgggttga cctcagtctc ctggagcttc cagccagagg 400
ggccgcacac tactgtgtcg ttttccact actccaagg gcaagtgtac 450
cttggaaatt atccaccatt taaagacaga atcagctggg ctggagacct 500
tgacaagaaa gatgcataa tcaacataga aaatatgcag tttatacaca 550
atggcaccta tatctgtat gtcaaaaacc ctccgtacat cggtgtccag 600
cctggacaca ttaggctcta tgtcgttagaa aaagagaatt tgcctgtgtt 650
tccagtttgg gtagtgtgg gcatagttac tgctgtggc ctaggtctca 700
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aaacgggatt acactggctg cagtacatca gagagttgt caccagttaa 800
cgaggctcct cggaaagtccc cctccgacac tgagggtctt gtaaagagtc 850
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tccggcggac atcacagtga caagattaac aagtcaaggt ctgtgggtgt 950
tgccgatatac cgaaagaatt aagagaatac ctggacata tcctcagcaa 1000

gaaacaaaac caaactggac tctcggtcag aaaatgttagc ccattaccac 1050
atgtgcctt ggagacccag gcaaggacaa gtacacgtgt actcacagag 1100
ggagagaaaag atgtgtacaa aggatatgtta taaatattct atttagtcat 1150
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caattggag atttcagaaa catttcatttc accatcattt agaaaatggtt 1300
tgccttaatg gagacaatag cagatcctgt agtattcca gtagacatgg 1350
ccttttaatc taaggccta agactgatta gtcttagcat ttactgttgt 1400
tggaggatgg agatgctatg atggaagcat acccagggtg gccttagca 1450
cagtatcgt accattttt tgtctgccgc ttttaaaaaa tacccattgg 1500
ctatgccact tgaaaacaat ttgagaagtt ttttgaagt ttttctcact 1550
aaaatatggg gcaattgtta gccttacatg ttgttagac ttactttaag 1600
tttgcaccct taaaatgtgt catatcaatt tctggattca taatagcaag 1650
attagcaaag gataaatgcc gaaggtcaact tcattctgga cacagttgga 1700
tcaatactga ttaagttagaa aatccaagct ttgcttgaga acttttgtaa 1750
cgtggagagt aaaaagtatc ggtttta 1777

<210> 364

<211> 269

<212> PRT

<213> Homo sapiens

<400> 364

Met Ala Ala Ser Ala Gly Ala Gly Ala Val Ile Ala Ala Pro Asp
1 5 10 15

Ser Arg Arg Trp Leu Trp Ser Val Leu Ala Ala Ala Leu Gly Leu
20 25 30

Leu Thr Ala Gly Val Ser Ala Leu Glu Val Tyr Thr Pro Lys Glu
35 40 45

Ile Phe Val Ala Asn Gly Thr Gln Gly Lys Leu Thr Cys Lys Phe
50 55 60

Lys Ser Thr Ser Thr Gly Gly Leu Thr Ser Val Ser Trp Ser
65 70 75

Phe Gln Pro Glu Gly Ala Asp Thr Thr Val Ser Phe Phe His Tyr
80 85 90

Ser Gln Gly Gln Val Tyr Leu Gly Asn Tyr Pro Pro Phe Lys Asp
95 100 105

Arg Ile Ser Trp Ala Gly Asp Leu Asp Lys Lys Asp Ala Ser Ile
110 115 120

Asn Ile Glu Asn Met Gln Phe Ile His Asn Gly Thr Tyr Ile Cys
125 130 135

Asp Val Lys Asn Pro Pro Asp Ile Val Val Gln Pro Gly His Ile
140 145 150

Arg Leu Tyr Val Val Glu Lys Glu Asn Leu Pro Val Phe Pro Val
155 160 165

Trp Val Val Val Gly Ile Val Thr Ala Val Val Leu Gly Leu Thr
170 175 180

Leu Leu Ile Ser Met Ile Leu Ala Val Leu Tyr Arg Arg Lys Asn
185 190 195

Ser Lys Arg Asp Tyr Thr Gly Cys Ser Thr Ser Glu Ser Leu Ser
200 205 210

Pro Val Lys Gln Ala Pro Arg Lys Ser Pro Ser Asp Thr Glu Gly
215 220 225

Leu Val Lys Ser Leu Pro Ser Gly Ser His Gln Gly Pro Val Ile
230 235 240

Tyr Ala Gln Leu Asp His Ser Gly Gly His His Ser Asp Lys Ile
245 250 255

Asn Lys Ser Glu Ser Val Val Tyr Ala Asp Ile Arg Lys Asn
260 265

<210> 365
<211> 1321
<212> DNA
<213> Homo sapiens

<400> 365
gccggctgtg cagagacgcc atgtaccggc tcctgtcagc agtgactgcc 50
cgggctgccg cccccggggg ctgggcctca agctgcggac gacgcggggt 100
ccatcagcgc gccgggctgc cgcccttcgg ccacggctgg gtcgggggcc 150
tcgggctggg gctggggctg gcgctcgaaa tgaagctggc aggtgggctg 200
aggggcgcgg ccccgccgca gtcccccgcg gcccccgacc ctgaggcgtc 250
gcctctggcc gagccgccac aggagcagtc cctcgcccg tggctccgc 300
agaccccgac gcccgcctgc tccaggtgct tcgccagagc catcgagagc 350
agccgcgacc tgctgcacag gatcaaggat gaggtggcgc caccggcat 400

agtggttgga gtttctgttag atggaaaaga agtctggtca gaaggtttag 450
gttatgctga ttttggagaac cgtgtaccat gtaaaccaga gacagttatg 500
cgaattgcta gcatcagcaa aagtctcacc atggttgctc ttgccaaatt 550
gtgggaagca gggaaactgg atcttgatataccatgacaa cattatgttc 600
ccgaattccc agaaaaagaa tatgaaggtg aaaaggttc tgtcacaaca 650
agattactga tttcccattt aagtggatt cgtcattatg aaaaggacat 700
aaaaaaaggtg aaagaagaga aagcttataa agccttgaag atgatgaaag 750
agaatgtgc atttgagcaa gaaaaagaag gcaaaagtaa tgaaaagaat 800
gattttacta aatttaaaac agagcaggag aatgaagcca aatgccggaa 850
ttcaaaaacct ggcaagaaaa agaatgattt tgaacaaggc gaattatatt 900
tgagagaaaa gtttggaaat tcaattgaat ccctaagatt atttaaaaat 950
gatccttgt tcttcaaacc tggtagtcag ttttgtatt caactttgg 1000
ctatacccta ctggcagcca tagtagagag agcttcagga tgtaaatatt 1050
tggactatat gcagaaaaata ttccatgact tggatatgct gacgactgtg 1100
caggaagaaa acgagccagt gatttacaat agagcaaggt aaatgaatac 1150
cttctgctgt gtctagctat atcgcatctt aacactatatt tattaattaa 1200
aagtcaaatt ttctttgtt ccattccaaa atcaacctgc cacatgg 1250
gagctttct acatgtctgt tttctcatct gtaaagtcaa ggaagtaaaa 1300
catgtttata aagtaaaaaa a 1321

<210> 366
<211> 373
<212> PRT
<213> Homo sapiens

<400> 366
Met Tyr Arg Leu Leu Ser Ala Val Thr Ala Arg Ala Ala Ala Pro
1 5 10 15
Gly Gly Leu Ala Ser Ser Cys Gly Arg Arg Gly Val His Gln Arg
20 25 30
Ala Gly Leu Pro Pro Leu Gly His Gly Trp Val Gly Gly Leu Gly
35 40 45
Leu Gly Leu Gly Leu Ala Leu Gly Val Lys Leu Ala Gly Gly Leu
50 55 60

Arg Gly Ala Ala Pro Ala Gln Ser Pro Ala Ala Pro Asp Pro Glu
65 70 75

Ala Ser Pro Leu Ala Glu Pro Pro Gln Glu Gln Ser Leu Ala Pro
80 85 90

Trp Ser Pro Gln Thr Pro Ala Pro Pro Cys Ser Arg Cys Phe Ala
95 100 105

Arg Ala Ile Glu Ser Ser Arg Asp Leu Leu His Arg Ile Lys Asp
110 115 120

Glu Val Gly Ala Pro Gly Ile Val Val Gly Val Ser Val Asp Gly
125 130 135

Lys Glu Val Trp Ser Glu Gly Leu Gly Tyr Ala Asp Val Glu Asn
140 145 150

Arg Val Pro Cys Lys Pro Glu Thr Val Met Arg Ile Ala Ser Ile
155 160 165

Ser Lys Ser Leu Thr Met Val Ala Leu Ala Lys Leu Trp Glu Ala
170 175 180

Gly Lys Leu Asp Leu Asp Ile Pro Val Gln His Tyr Val Pro Glu
185 190 195

Phe Pro Glu Lys Glu Tyr Glu Gly Glu Lys Val Ser Val Thr Thr
200 205 210

Arg Leu Leu Ile Ser His Leu Ser Gly Ile Arg His Tyr Glu Lys
215 220 225

Asp Ile Lys Lys Val Lys Glu Glu Lys Ala Tyr Lys Ala Leu Lys
230 235 240

Met Met Lys Glu Asn Val Ala Phe Glu Gln Glu Lys Glu Gly Lys
245 250 255

Ser Asn Glu Lys Asn Asp Phe Thr Lys Phe Lys Thr Glu Gln Glu
260 265 270

Asn Glu Ala Lys Cys Arg Asn Ser Lys Pro Gly Lys Lys Lys Asn
275 280 285

Asp Phe Glu Gln Gly Glu Leu Tyr Leu Arg Glu Lys Phe Glu Asn
290 295 300

Ser Ile Glu Ser Leu Arg Leu Phe Lys Asn Asp Pro Leu Phe Phe
305 310 315

Lys Pro Gly Ser Gln Phe Leu Tyr Ser Thr Phe Gly Tyr Thr Leu
320 325 330

Leu Ala Ala Ile Val Glu Arg Ala Ser Gly Cys Lys Tyr Leu Asp
335 340 345

Tyr Met Gln Lys Ile Phe His Asp Leu Asp Met Leu Thr Thr Val
350 355 360

Gln Glu Glu Asn Glu Pro Val Ile Tyr Asn Arg Ala Arg
365 370

<210> 367
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 367
tggaaaagaa gtctggtcag aagggttagg 30

<210> 368
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 368
cattggctt cattctccctg ctctg 25

<210> 369
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 369
aaaacacctag aacaactcat tttgcacc 28

<210> 370
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 370
gtctcaccat ggttgctt gccaattgt ggaaaggcagg g 41

<210> 371
<211> 1150
<212> DNA
<213> Homo sapiens

<400> 371
gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 50

gaattcggct cgaggctggt gggagaagc cgagatggcg gcagccagcg 100
ctggggcaac ccggctgctc ctgctttgc tcatggcggt agcagcgccc 150
agtgcagccc gggcagcgg ctgccgggcc gggactggtg cgcgagggc 200
tggggcgaa ggtcgagagg gcgaggcctg tggcacggtg gggctgctgc 250
tggagcactc atttagatc gatgacagtg ccaacttccg gaagcgggc 300
tcactgctct ggaaccagca ggatggtacc ttgtccctgt cacagcggca 350
gctcagcggag gaggagcggg gccgactccg ggatgtggca gccctgaatg 400
gcctgtaccg ggtccggatc ccaaggcgac ccggggccct ggatggcctg 450
gaagctggtg gctatgtctc ctcccttgtc cctgcgtgt ccctggtgga 500
gtcgacactg tcggaccagc tgaccctgca cgtggatgtg gccggcaacg 550
tggggcggt gtcgggtgt acgcaccccg gggctgccc gggccatgag 600
gtggaggacg tggacctgga gctgttcaac acctcggtgc agctgcagcc 650
gccaccaca gccccaggcc ctgagacggc ggccttcatt gagcgcctgg 700
agatgaaaca gccccagaag gccaagaacc cccaggagca gaagtccttc 750
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ttaaaaacat cgacgataca ttgaaatgtg tgaacgttt gaaaagctac 950
agcttccagc agccaaaagc aactgttgtt ttggcaagac ggtcctgatg 1000
tacaagctt attgaaattc actgctcact tgatacgtta ttcagaaacc 1050
caaggaatgg ctgtcccat cctcatgtgg ctgtgtggag ctcagctgtg 1100
ttgtgtggca gtttattaaa ctgtccccca gatcgacacg caaaaaaaaa 1150

<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met	Ala	Ala	Ala	Ser	Ala	Gly	Ala	Thr	Arg	Leu	Leu	Leu	Leu	Leu
1										10				15

Leu	Met	Ala	Val	Ala	Ala	Pro	Ser	Arg	Ala	Arg	Gly	Ser	Gly	Cys
														30
						20				25				

Arg	Ala	Gly	Thr	Gly	Ala	Arg	Gly	Ala	Glu	Gly	Arg	Glu		
					35			40				45		
Gly	Glu	Ala	Cys	Gly	Thr	Val	Gly	Leu	Leu	Leu	Glu	His	Ser	Phe
					50			55				60		
Glu	Ile	Asp	Asp	Ser	Ala	Asn	Phe	Arg	Lys	Arg	Gly	Ser	Leu	Leu
					65			70				75		
Trp	Asn	Gln	Gln	Asp	Gly	Thr	Leu	Ser	Leu	Ser	Gln	Arg	Gln	Leu
					80			85				90		
Ser	Glu	Glu	Glu	Arg	Gly	Arg	Leu	Arg	Asp	Val	Ala	Ala	Leu	Asn
					95			100				105		
Gly	Leu	Tyr	Arg	Val	Arg	Ile	Pro	Arg	Arg	Pro	Gly	Ala	Leu	Asp
					110			115				120		
Gly	Leu	Glu	Ala	Gly	Gly	Tyr	Val	Ser	Ser	Phe	Val	Pro	Ala	Cys
					125			130				135		
Ser	Leu	Val	Glu	Ser	His	Leu	Ser	Asp	Gln	Leu	Thr	Leu	His	Val
					140			145				150		
Asp	Val	Ala	Gly	Asn	Val	Val	Gly	Val	Ser	Val	Val	Thr	His	Pro
					155			160				165		
Gly	Gly	Cys	Arg	Gly	His	Glu	Val	Glu	Asp	Val	Asp	Leu	Glu	Leu
					170			175				180		
Phe	Asn	Thr	Ser	Val	Gln	Leu	Gln	Pro	Pro	Thr	Thr	Ala	Pro	Gly
					185			190				195		
Pro	Glu	Thr	Ala	Ala	Phe	Ile	Glu	Arg	Leu	Glu	Met	Glu	Gln	Ala
					200			205				210		
Gln	Lys	Ala	Lys	Asn	Pro	Gln	Glu	Gln	Lys	Ser	Phe	Phe	Ala	Lys
					215			220				225		
Tyr	Trp	Met	Tyr	Ile	Ile	Pro	Val	Val	Leu	Phe	Leu	Met	Met	Ser
					230			235				240		
Gly	Ala	Pro	Asp	Thr	Gly	Gly	Gln	Gly						
					245			250				255		
Gly	Gly	Gly	Gly	Ser	Gly	Leu	Cys	Cys	Val	Pro	Pro	Ser	Leu	
					260			265						

<210> 373

<211> 1706

<212> DNA

<213> Homo sapiens

<400> 373

ggagcgctgc tggaaacccga gccggagccg gagccacagc ggggagggtg 50

gcctggcggc ctggagccgg acgtgtccgg ggcgtccccg cagaccgggg 100

cagcaggctcg tccgggggcc caccatgctg gtgactgcct accttgcttt 150
tgtaggcctc ctggcctcct gcctggggct ggaactgtca agatgccggg 200
ctaaaccccc tggaaggggcc tgcagcaatc ctccttcct tcggtttcaa 250
ctggacttct atcaggtcta cttcctggcc ctggcagctg attggcttca 300
ggccccctac ctctataaac tctaccagca ttactacttc ctggaaggtc 350
aaattgccat cctctatgtc tgtggccttg cctctacagt cctctttggc 400
ctagtggcct ctccttctgt ggattggctg ggtcgcaaga attcttgtgt 450
cctcttctcc ctgacttact cactatgctg cttAACAAA ctctctcaag 500
actactttgt gctgcttagtg gggcgagcac ttgggtggct gtccacagcc 550
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gcatgacttc cctgctgagt ggatcccagc taccttgct cgagctgcct 650
tctggaacca tgtgctggct gtagtggcag gtgtggcagc tgaggctgta 700
gccagctgga tagggctggg gcctgttagcg cccttggct ctgcatccc 750
tctcctggct ctggcagggg ccttggccct tcgaaactgg ggggagaact 800
atgaccggca gcgtgccttc tcaaggacct gtgctggagg cctgcgctgc 850
ctcctgtcgg accgcccgcgt gctgctgctg ggcaccatac aagctctatt 900
tgagagtgtc atcttcatct ttgtcttcct ctggacacct gtgctggacc 950
cacacggggc ccctctggc attatcttct ccagttcat ggcagccagc 1000
ctgcttggct ctcccctgta ccgtatcgcc acctccaaga ggtaccacct 1050
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tcttcatgtt gactttctct accagccccag gccaggagag tccgggtggag 1150
tccttcatag cctttctact tattgagttg gcttggat tatactttcc 1200
cagcatgagc ttcctacgga gaaagggtat ccctgagaca gagcaggctg 1250
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ctccttgc tccatgacag tgatcgaaaa acaggcactc ggaatatgtt 1350
cagcatttgc tctgctgtca tggtgatggc tctgctggca gtgggtggac 1400
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gaggagccct atgcccctga gctgtaaaccc cactccagga caagatagct 1500

gggacagact cttgaattcc agctatccgg gattgtacag atctctctgt 1550
gactgacttt gtgactgtcc tgtggtttct cctgccattg ctttgtgtt 1600
gggaggacat gatgggggtg atggactgga aagaaggtgc caaaagtcc 1650
ctctgtgtta ctcccattta gaaaataaac acttttaaat gatcaaaaaa 1700
aaaaaa 1706

<210> 374

<211> 450

<212> PRT

<213> Homo sapiens

<400> 374

Met Leu Val Thr Ala Tyr Leu Ala Phe Val Gly Leu Leu Ala Ser
1 5 10 15

Cys Leu Gly Leu Glu Leu Ser Arg Cys Arg Ala Lys Pro Pro Gly
20 25 30

Arg Ala Cys Ser Asn Pro Ser Phe Leu Arg Phe Gln Leu Asp Phe
35 40 45

Tyr Gln Val Tyr Phe Leu Ala Leu Ala Asp Trp Leu Gln Ala
50 55 60

Pro Tyr Leu Tyr Lys Leu Tyr Gln His Tyr Tyr Phe Leu Glu Gly
65 70 75

Gln Ile Ala Ile Leu Tyr Val Cys Gly Leu Ala Ser Thr Val Leu
80 85 90

Phe Gly Leu Val Ala Ser Ser Leu Val Asp Trp Leu Gly Arg Lys
95 100 105

Asn Ser Cys Val Leu Phe Ser Leu Thr Tyr Ser Leu Cys Cys Leu
110 115 120

Thr Lys Leu Ser Gln Asp Tyr Phe Val Leu Leu Val Gly Arg Ala
125 130 135

Leu Gly Gly Leu Ser Thr Ala Leu Leu Phe Ser Ala Phe Glu Ala
140 145 150

Trp Tyr Ile His Glu His Val Glu Arg His Asp Phe Pro Ala Glu
155 160 165

Trp Ile Pro Ala Thr Phe Ala Arg Ala Ala Phe Trp Asn His Val
170 175 180

Leu Ala Val Val Ala Gly Val Ala Ala Glu Ala Val Ala Ser Trp
185 190 195

Ile Gly Leu Gly Pro Val Ala Pro Phe Val Ala Ala Ile Pro Leu
200 205 210

Leu Ala Leu Ala Gly Ala Leu Ala Leu Arg Asn Trp Gly Glu Asn
215 220 225

Tyr Asp Arg Gln Arg Ala Phe Ser Arg Thr Cys Ala Gly Gly Leu
230 235 240

Arg Cys Leu Leu Ser Asp Arg Arg Val Leu Leu Leu Gly Thr Ile
245 250 255

Gln Ala Leu Phe Glu Ser Val Ile Phe Ile Phe Val Phe Leu Trp
260 265 270

Thr Pro Val Leu Asp Pro His Gly Ala Pro Leu Gly Ile Ile Phe
275 280 285

Ser Ser Phe Met Ala Ala Ser Leu Leu Gly Ser Ser Leu Tyr Arg
290 295 300

Ile Ala Thr Ser Lys Arg Tyr His Leu Gln Pro Met His Leu Leu
305 310 315

Ser Leu Ala Val Leu Ile Val Val Phe Ser Leu Phe Met Leu Thr
320 325 330

Phe Ser Thr Ser Pro Gly Gln Glu Ser Pro Val Glu Ser Phe Ile
335 340 345

Ala Phe Leu Leu Ile Glu Leu Ala Cys Gly Leu Tyr Phe Pro Ser
350 355 360

Met Ser Phe Leu Arg Arg Lys Val Ile Pro Glu Thr Glu Gln Ala
365 370 375

Gly Val Leu Asn Trp Phe Arg Val Pro Leu His Ser Leu Ala Cys
380 385 390

Leu Gly Leu Leu Val Leu His Asp Ser Asp Arg Lys Thr Gly Thr
395 400 405

Arg Asn Met Phe Ser Ile Cys Ser Ala Val Met Val Met Ala Leu
410 415 420

Leu Ala Val Val Gly Leu Phe Thr Val Val Arg His Asp Ala Glu
425 430 435

Leu Arg Val Pro Ser Pro Thr Glu Glu Pro Tyr Ala Pro Glu Leu
440 445 450

<210> 375

<211> 1098

<212> DNA

<213> Homo sapiens

<400> 375

gcgacgcgcg gcggggcgcc gagaggaaac gcggcgccgg gccggggcccg 50

gccctggaga tggtccccgg cgccgcgggc tggtgttgc tcgtgctcg 100
gctccccgcg tgcgtcgccg cccacggctt ccgtatccat gattattgt 150
actttcaagt gctgagtcct ggggacattc gatacatctt cacagccaca 200
cctgccaagg actttggtgg tatcttcac acaaggtatg agcagattca 250
ccttgcccc gctgaacctc cagaggcctg cggggaaactc agcaacggtt 300
tcttcatcca ggaccagatt gctctggtgg agaggggggg ctgctccttc 350
ctctccaaga ctcgggtgg ccaggagcac ggcgggcggg cggtgatcat 400
ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450
acagtacccā gcgcacagct gacatccccg ccctttcct gctcgccga 500
gacggctaca tgatccgccc ctctctggaa cagcatggc tgccatggc 550
catcatttcc atcccagtca atgtcaccag catccccacc tttgagctgc 600
tgcaaccgco ctggaccttc tggtagaaga gtttgcctt cattccagcc 650
ataagtgact ctgagctgg aaggggaaac ccaggaattt tgctacttgg 700
aatttggaga tagcatctgg ggacaagtgg agccaggtag aggaaaagg 750
tttggcggt gctaggctga aagggaaagcc acaccactgg cttcccttc 800
cccagggccc ccaagggtgt ctcatgctac aagaagaggc aagagacagg 850
ccccagggtct tctggctaga acccgaaaca aaaggagctg aaggcaggtg 900
gcctgagagc catctgtgac ctgtcacact cacctggctc cagcctcccc 950
tacccagggt ctctgcacag tgaccttcac agcagttgtt ggagtggttt 1000
aaagagctgg tgtttggga ctcaataaac cctcaactgac ttttagcaa 1050
taaagcttct catcagggtt gcaaaaaaaaaaaaaaaa 1098

<210> 376
<211> 188
<212> PRT
<213> Homo sapiens

<400> 376
Met Val Pro Gly Ala Ala Gly Trp Cys Cys Leu Val Leu Trp Leu
1 5 10 15
Pro Ala Cys Val Ala Ala His Gly Phe Arg Ile His Asp Tyr Leu
20 25 30
Tyr Phe Gln Val Leu Ser Pro Gly Asp Ile Arg Tyr Ile Phe Thr
35 40 45

Ala Thr Pro Ala Lys Asp Phe Gly Gly Ile Phe His Thr Arg Tyr
50 55 60

Glu Gln Ile His Leu Val Pro Ala Glu Pro Pro Glu Ala Cys Gly
65 70 75

Glu Leu Ser Asn Gly Phe Phe Ile Gln Asp Gln Ile Ala Leu Val
80 85 90

Glu Arg Gly Gly Cys Ser Phe Leu Ser Lys Thr Arg Val Val Gln
95 100 105

Glu His Gly Gly Arg Ala Val Ile Ile Ser Asp Asn Ala Val Asp
110 115 120

Asn Asp Ser Phe Tyr Val Glu Met Ile Gln Asp Ser Thr Gln Arg
125 130 135

Thr Ala Asp Ile Pro Ala Leu Phe Leu Leu Gly Arg Asp Gly Tyr
140 145 150

Met Ile Arg Arg Ser Leu Glu Gln His Gly Leu Pro Trp Ala Ile
155 160 165

Ile Ser Ile Pro Val Asn Val Thr Ser Ile Pro Thr Phe Glu Leu
170 175 180

Leu Gln Pro Pro Trp Thr Phe Trp
185

<210> 377
<211> 496
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 396
<223> unknown base

<400> 377
tctgcctcca ctgctctgtg ctgggatcat ggaacttgca ctgctgtgtg 50
ggctggtgtt gatggcttgtt gtgattccaa tccagggcgg gatcctgaac 100
ctgaacaaga tggtaagca agtgactggg aaaatgccca tccttcctta 150
ctggccctac ggctgtcact gcggacttagg tggcagaggc caacccaaag 200
atgccacgga ctggtgctgc cagacccatg actgctgcta tgaccacctg 250
aagacccagg ggtgcggcat ctacaaggac aacaacaaaa gcagcataca 300
ttgtatggat ttatctcaac gctattgttt aatggctgtg ttatgtga 350
tctatctgga aaatgaggac tccgaataaa aagctattac tawtnaaaa 400

aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa 450

aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaa 496

<210> 378

<211> 116

<212> PRT

<213> Homo sapiens

<400> 378

Met Glu Leu Ala Leu Leu Cys Gly Leu Val Val Met Ala Gly Val
1 5 10 15

Ile Pro Ile Gln Gly Gly Ile Leu Asn Leu Asn Lys Met Val Lys
20 25 30

Gln Val Thr Gly Lys Met Pro Ile Leu Ser Tyr Trp Pro Tyr Gly
35 40 45

Cys His Cys Gly Leu Gly Gly Arg Gly Gln Pro Lys Asp Ala Thr
50 55 60

Asp Trp Cys Cys Gln Thr His Asp Cys Cys Tyr Asp His Leu Lys
65 70 75

Thr Gln Gly Cys Gly Ile Tyr Lys Asp Asn Asn Lys Ser Ser Ile
80 85 90

His Cys Met Asp Leu Ser Gln Arg Tyr Cys Leu Met Ala Val Phe
95 100 105

Asn Val Ile Tyr Leu Glu Asn Glu Asp Ser Glu
110 115

<210> 379

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 379

ctgcctccac tgctctgtgc tggg 24

<210> 380

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 380

cagagcagtg gatgttcccc tggg 24

<210> 381

<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 381
ctgaacaaga tggtaagca agtgactggg aaaatgccc tcctc 45

<210> 382
<211> 764
<212> DNA
<213> Homo sapiens

<400> 382
ctcgcttctt cttctggat gggggcccaag ggggcccagg agagtataaa 50
ggcgatgtgg agggtgcccg gcacaaccag acgcccagtc acaggcgaga 100
gcacctggat gcaccggcca gaggccatgc tgctgctgct cacgcttgcc 150
ctcctgggg gccccacctg ggcaggaaag atgtatggcc ctggaggagg 200
caagtatttc agcaccactg aagactacga ccatgaaatc acagggctgc 250
gggtgtctgt aggtcttctc ctggtaaaaa gtgtccaggt gaaacttgg 300
gactcctggg acgtgaaaact gggagcctta ggtggaaata cccaggaagt 350
cacccctgcag ccaggcgaat acatcacaaa agtcttgtc gccttccaag 400
cttcctccg gggatggtc atgtacacca gcaaggaccg ctatttctat 450
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gcaggtgctg gtggcataat atggccagta tcaactcctt ggcataaga 550
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ccagttaatc tcacataactc agcaaactca cccgtgggtc gctagggtgg 650
ggtatgggc catccgagct gaggccatct gtgtgggtgt ggctgatgg 700
actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750
gcttctgcag aaaa 764

<210> 383
<211> 178
<212> PRT
<213> Homo sapiens

<400> 383
Met His Arg Pro Glu Ala Met Leu Leu Leu Leu Thr Leu Ala Leu
1 5 10 15

Leu	Gly	Gly	Pro	Thr	Trp	Ala	Gly	Lys	Met	Tyr	Gly	Pro	Gly	Gly
			20					25				30		
Gly	Lys	Tyr	Phe	Ser	Thr	Thr	Glu	Asp	Tyr	Asp	His	Glu	Ile	Thr
	35						40					45		
Gly	Leu	Arg	Val	Ser	Val	Gly	Leu	Leu	Leu	Val	Lys	Ser	Val	Gln
			50					55				60		
Val	Lys	Leu	Gly	Asp	Ser	Trp	Asp	Val	Lys	Leu	Gly	Ala	Leu	Gly
	65						70					75		
Gly	Asn	Thr	Gln	Glu	Val	Thr	Leu	Gln	Pro	Gly	Glu	Tyr	Ile	Thr
	80						85					90		
Lys	Val	Phe	Val	Ala	Phe	Gln	Ala	Phe	Leu	Arg	Gly	Met	Val	Met
	95						100					105		
Tyr	Thr	Ser	Lys	Asp	Arg	Tyr	Phe	Tyr	Phe	Gly	Lys	Leu	Asp	Gly
	110						115					120		
Gln	Ile	Ser	Ser	Ala	Tyr	Pro	Ser	Gln	Glu	Gly	Gln	Val	Leu	Val
	125						130					135		
Gly	Ile	Tyr	Gly	Gln	Tyr	Gln	Leu	Leu	Gly	Ile	Lys	Ser	Ile	Gly
	140						145					150		
Phe	Glu	Trp	Asn	Tyr	Pro	Leu	Glu	Glu	Pro	Thr	Thr	Glu	Pro	Pro
	155						160					165		
Val	Asn	Leu	Thr	Tyr	Ser	Ala	Asn	Ser	Pro	Val	Gly	Arg		
	170						175							

<210> 384
<211> 2379
<212> DNA
<213> Homo sapiens

<400> 384
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agctctgtgg ctgaactggg tgctcatcac ggaaactgct gggctatgga 100
atacagatgt ggcagctca gtagccccaa attgcctgga agaatacatac 150
atgttttcg ataagaagaa attgtaggat ccagttttt ttttaaccgc 200
ccccctccca ccccccaaaa aaactgtaaa gatgaaaaaa cgtaatatcc 250
atgaagatcc tattacctag gaagatttg atgtttgct gcgaatgcgg 300
tgttgggatt tatttgtct tggagtgttc tgcgtggctg gcaaagaata 350
atgttccaaa atcggtccat ctcccaaggg gtccaaattt tcttcctgg 400
tgtcagcgag ccctgactca ctacagtgca gctgacaggg gctgtcatgc 450

aactggcccc taagccaaag caaaagacct aaggacgacc tttgaacaat 500
acaaaggatg ggtttcaatg taattaggct actgagcgga tcagctgtag 550
cactggttat agccccact gtcttactga caatgcttc ttctgccaa 600
cgaggatgcc ctaaggcgtg taggtgtgaa ggcaaaatgg tatattgtga 650
atctcagaaa ttacaggaga taccctcaag tataatctgct ggttgcttag 700
gtttagtccct tcgctataac agccttcaaa aacttaagta taatcaattt 750
aaagggctca accagctcac ctggctatac cttgaccata accatatcag 800
caatattgac gaaaatgctt ttaatgaaat acgcagactc aaagagctga 850
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gtgacaaatt tacggaactt ggatctgtcc tataatcagc tgcattctct 950
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ggctctaactc cctgagaacc atccctgtgc gaatattcca agactgccgc 1050
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aatgtcttt gctggcatga tcagactcaa agaacttcac ctggagcaca 1150
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aatgcagcag aaatatttgc tcccttgtaa actggctgaa aagttttaaa 1500
ggctctaagg agaatacaat tatctgtgcc agtcccaaag agctgcaagg 1550
agtaaatgtg atcgatgcag tgaagaacta cagcatctgt ggcaaaagta 1600
ctacagagag gtttgatctg gccagggctc tcccaaagcc gacgtttaag 1650
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ctcgtcatcc tgctggttat ctacgtgtca tggaaagcggt accctgcgag 1850
catgaagcag ctgcagcagc gctccctcat gcgaaggcac agaaaaaaga 1900

aaagacagtc cctaaagcaa atgactccca gcaccaggaa attttatgt 1950
gattataaac ccaccaacac ggagaccagc gagatgctgc tgaatggac 2000
gggaccctgc acctataaca aatcgggctc cagggagtgt gaggtatgaa 2050
ccattgtat aaaaagagct cttaaaagct gggaaataag tggtgctta 2100
ttgaactctg gtgactatca aggaaacgcg atgccccccc tccccctccc 2150
tctccctctc actttggtgg caagatcctt ccttgtccgt ttttagtgcat 2200
tcataatact ggtcatttc ctctcataca taatcaaccc attgaaattt 2250
aaataccaca atcaatgtga agcttgaact ccggttaat ataataccta 2300
ttgtataaga cccttactg attccattaa tgtcgcat ttttaagat 2350
aaaacttctt tcataaggtaa aaaaaaaaa 2379

<210> 385

<211> 513

<212> PRT

<213> Homo sapiens

<400> 385

Met Gly Phe Asn Val Ile Arg Leu Leu Ser Gly Ser Ala Val Ala
1 5 10 15

Leu Val Ile Ala Pro Thr Val Leu Leu Thr Met Leu Ser Ser Ala
20 25 30

Glu Arg Gly Cys Pro Lys Gly Cys Arg Cys Glu Gly Lys Met Val
35 40 45

Tyr Cys Glu Ser Gln Lys Leu Gln Glu Ile Pro Ser Ser Ile Ser
50 55 60

Ala Gly Cys Leu Gly Leu Ser Leu Arg Tyr Asn Ser Leu Gln Lys
65 70 75

Leu Lys Tyr Asn Gln Phe Lys Gly Leu Asn Gln Leu Thr Trp Leu
80 85 90

Tyr Leu Asp His Asn His Ile Ser Asn Ile Asp Glu Asn Ala Phe
95 100 105

Asn Gly Ile Arg Arg Leu Lys Glu Leu Ile Leu Ser Ser Asn Arg
110 115 120

Ile Ser Tyr Phe Leu Asn Asn Thr Phe Arg Pro Val Thr Asn Leu
125 130 135

Arg Asn Leu Asp Leu Ser Tyr Asn Gln Leu His Ser Leu Gly Ser
140 145 150

Glu Gln Phe Arg Gly Leu Arg Lys Leu Leu Ser Leu His Leu Arg
155 160 165

Ser Asn Ser Leu Arg Thr Ile Pro Val Arg Ile Phe Gln Asp Cys
170 175 180

Arg Asn Leu Glu Leu Leu Asp Leu Gly Tyr Asn Arg Ile Arg Ser
185 190 195

Leu Ala Arg Asn Val Phe Ala Gly Met Ile Arg Leu Lys Glu Leu
200 205 210

His Leu Glu His Asn Gln Phe Ser Lys Leu Asn Leu Ala Leu Phe
215 220 225

Pro Arg Leu Val Ser Leu Gln Asn Leu Tyr Leu Gln Trp Asn Lys
230 235 240

Ile Ser Val Ile Gly Gln Thr Met Ser Trp Thr Trp Ser Ser Leu
245 250 255

Gln Arg Leu Asp Leu Ser Gly Asn Glu Ile Glu Ala Phe Ser Gly
260 265 270

Pro Ser Val Phe Gln Cys Val Pro Asn Leu Gln Arg Leu Asn Leu
275 280 285

Asp Ser Asn Lys Leu Thr Phe Ile Gly Gln Glu Ile Leu Asp Ser
290 295 300

Trp Ile Ser Leu Asn Asp Ile Ser Leu Ala Gly Asn Ile Trp Glu
305 310 315

Cys Ser Arg Asn Ile Cys Ser Leu Val Asn Trp Leu Lys Ser Phe
320 325 330

Lys Gly Leu Arg Glu Asn Thr Ile Ile Cys Ala Ser Pro Lys Glu
335 340 345

Leu Gln Gly Val Asn Val Ile Asp Ala Val Lys Asn Tyr Ser Ile
350 355 360

Cys Gly Lys Ser Thr Thr Glu Arg Phe Asp Leu Ala Arg Ala Leu
365 370 375

Pro Lys Pro Thr Phe Lys Pro Lys Leu Pro Arg Pro Lys His Glu
380 385 390

Ser Lys Pro Pro Leu Pro Pro Thr Val Gly Ala Thr Glu Pro Gly
395 400 405

Pro Glu Thr Asp Ala Asp Ala Glu His Ile Ser Phe His Lys Ile
410 415 420

Ile Ala Gly Ser Val Ala Leu Phe Leu Ser Val Leu Val Ile Leu
425 430 435

Leu Val Ile Tyr Val Ser Trp Lys Arg Tyr Pro Ala Ser Met Lys
440 445 450
Gln Leu Gln Gln Arg Ser Leu Met Arg Arg His Arg Lys Lys Lys
455 460 465
Arg Gln Ser Leu Lys Gln Met Thr Pro Ser Thr Gln Glu Phe Tyr
470 475 480
Val Asp Tyr Lys Pro Thr Asn Thr Glu Thr Ser Glu Met Leu Leu
485 490 495
Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu
500 505 510
Cys Glu Val

<210> 386
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 386
ctggatctg aacagttcg gggc 24

<210> 387
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 387
ggtccccagg acatggtctg tccc 24

<210> 388
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 388
gctgagttta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389
<211> 1449
<212> DNA
<213> Homo sapiens

<400> 389

agtctgaga aagaaggaaa taaacacagg caccaaacca ctatcctaag 50
ttgactgtcc tttaaatatg tcaagatcca gactttcag tgtcacctca 100
gcgatctcaa cgataggat cttgttgg ccgctattcc agttggtgct 150
ctcgaccta ccatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200
aacaccctaa tggctggat atctggatcc tcctgctgct gttttgg 250
gcagctcttc tctgtggagc tgtggcctc tgcctccagt gctggctgag 300
gagaccccga attgattctc acaggcgcac catggcagtt tttgctgttg 350
gagacttgga ctctatttat gggacagaag cagctgtgag tccaactgtt 400
ggaattcacc ttcaaactca aacccctgac ctatatcctg ttcctgctcc 450
atgtttggc cctttaggct ccccacctcc atatgaagaa attgtaaaaa 500
caacctgatt ttaggtgtgg attatcaatt taaagtatta acgacatctg 550
taattccaaa acatcaaatt taggaatagt tatttcagtt gttggaaatg 600
tccagagatc tattcatata gtctgaggaa ggacaattcg acaaaagaat 650
ggatgttgga aaaaattttg gtcatggaga tgtttaata gtaaagtgc 700
aggctttga tgtgtcactg ctgtatcata cttttatgct acacaaccaa 750
attaatgctt ctccactagt atccaaacag gcaacaatta ggtgctggaa 800
gtagttcca tcacattnag gactccactg cagtatacag cacaccattt 850
tctgcttaa actcttcct agcatgggg ccataaaaat tattataatt 900
taacaatagc ccaagccgag aatccaacat gtccagaacc agaaccagaa 950
agatagtatt tgaatgaagg tgaggggaga gagtaggaaa aagaaaagtt 1000
tggagttgaa gggtaaagga taaatgaaga ggaaaaggaa aagattacaa 1050
gtctcagcaa aaacaagagg ttttatgcc caacctgaag aggaagaaat 1100
tgtagataga aggtgaagga gattgctgaa gatataagac acatataatg 1150
ccaacacggg gagaaaagaa aatttccccct tttacagtaa tgaatgtggc 1200
ctccatagtc catagtgttt ctctggagcc tcagggcttg gcattttatg 1250
cagcatcatg ctaagaacct tcggcatagg tatctgttcc catgaggact 1300
gcagaagtag caatgagaca tcttcaagtg gcattttggc agtggccatc 1350
agcagggggga cagacaaaaa catccatcac agatgacata tgatcttcag 1400
ctgacaaatt tggtgaacaa aacaataaac atcaatagat atctaaaaa 1449

<210> 390
<211> 146
<212> PRT
<213> Homo sapiens

<400> 390
Met Ser Arg Ser Arg Leu Phe Ser Val Thr Ser Ala Ile Ser Thr
1 5 10 15

Ile Gly Ile Leu Cys Leu Pro Leu Phe Gln Leu Val Leu Ser Asp
20 25 30

Leu Pro Cys Glu Glu Asp Glu Met Cys Val Asn Tyr Asn Asp Gln
35 40 45

His Pro Asn Gly Trp Tyr Ile Trp Ile Leu Leu Leu Leu Val Leu
50 55 60

Val Ala Ala Leu Leu Cys Gly Ala Val Val Leu Cys Leu Gln Cys
65 70 75

Trp Leu Arg Arg Pro Arg Ile Asp Ser His Arg Arg Thr Met Ala
80 85 90

Val Phe Ala Val Gly Asp Leu Asp Ser Ile Tyr Gly Thr Glu Ala
95 100 105

Ala Val Ser Pro Thr Val Gly Ile His Leu Gln Thr Gln Thr Pro
110 115 120

Asp Leu Tyr Pro Val Pro Ala Pro Cys Phe Gly Pro Leu Gly Ser
125 130 135

Pro Pro Pro Tyr Glu Glu Ile Val Lys Thr Thr
140 145

<210> 391
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 391
ctttcagtg tcacccatgc gatctc 26

<210> 392
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 392

ccaaaacatg gagcaggaac agg 23
<210> 393
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 393
ccagttggtg ctctcgacc taccatgcga agaagatgaa atgtgtg 47

<210> 394
<211> 2340
<212> DNA
<213> Homo sapiens

<400> 394
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acccacccgc gtttctccag ctcgatctgg aggctgcttc gccagtgtgg 100
gacgcagctg acgccccgtt attagctctc gctgcgtcgc cccggctcag 150
aagctccgtg gcggcggcga ccgtgacgag aagcccacgg ccagctcagt 200
tctcttctac tttgggagag agagaaaagtc agatgcccct tttaaactcc 250
ctcttcaaaa ctcatctcct gggtgactga gttaatagag tggataacaac 300
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gtctgttgtt ttgcttcttc agaaatgttt tttacaatct caagaaaaaa 450
tatgtcccag aaattgagtt tactgttgct tgtatttggg ctcatttggg 500
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cagtaaccac aaataaaaaga acgaatgtct cggcagttt cagatagcag 850
ttgaaaatca ccttgtgctg ctccatccac tgtggattat atcctatggc 900
agaaaagctt tataattgct ggcttaggac agagcaatac tttacaataa 950

aagctctaca cattttcaag gagtatgctg gattcatgga actctaattc 1000
tgtacataaa aattttaaag ttatttgaaa gcttcaggc aagtctgttc 1050
aatgctgtac tatgtcctta aagagaattt ggtaacttgg ttgatgtggt 1100
aagcagatag gtgagtttg tataaatctt ttgtgttga gatcaagctg 1150
aatgaaaac actgaaaaac atggattcat ttctataaca catttattta 1200
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tatgaagatt gactatctt tcaggaaaaaa agctgtatatac agcacaggaa 2000
accctaatttct tggtaatttct aattgccaca tggtgcctta tatttcata 2050
atttcccttgc tagcaaatttct aattgccaca tggtgcctta tatttcata 2100
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actatataaga atttagatatac ttttgcatttgc ttttgcatttgc 2200
catgttagcaa taatttacaat attttattaa aataaatatg tgaaatattg 2250
tttcatgaaa gacagatttcc caaatctctc ttctcttctc ttttgcatttgc 2300
acctttatgttgc gaagaaatatttgc attatatgttgc atttgcatttgc 2340

<211> 140
<212> PRT
<213> Homo sapiens

<400> 395

Met Phe Phe Thr Ile Ser Arg Lys Asn Met Ser Gln Lys Leu Ser
1 5 10 15
Leu Leu Leu Leu Val Phe Gly Leu Ile Trp Gly Leu Met Leu Leu
20 25 30
His Tyr Thr Phe Gln Gln Pro Arg His Gln Ser Ser Val Lys Leu
35 40 45
Arg Glu Gln Ile Leu Asp Leu Ser Lys Arg Tyr Val Lys Ala Leu
50 55 60
Ala Glu Glu Asn Lys Asn Thr Val Asp Val Glu Asn Gly Ala Ser
65 70 75
Met Ala Gly Tyr Ala Asp Leu Lys Arg Thr Ile Ala Val Leu Leu
80 85 90
Asp Asp Ile Leu Gln Arg Leu Val Lys Leu Glu Asn Lys Val Asp
95 100 105
Tyr Ile Val Val Asn Gly Ser Ala Ala Asn Thr Thr Asn Gly Thr
110 115 120
Ser Gly Asn Leu Val Pro Val Thr Thr Asn Lys Arg Thr Asn Val
125 130 135
Ser Gly Ser Ile Arg
140

<210> 396
<211> 2639
<212> DNA
<213> Homo sapiens

<400> 396

cgcggccggg cgcgggggt gagcgtgccg aggcgctgt ggcgcaggct 50
tccagcccccc accatgccgt ggccccctgct gctgctgctg gccgtgagtg 100
ggggccagac aaccggcca tgctccccg ggtgccaatg cgaggtggag 150
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cctggggccc cacatcatgc cggtgccccat ccctctggac acagcccact 250
tggacctgtc ctccaaccgg ctggagatgg tgaatgagtc ggtgttggcg 300
ggggcgggct acacgacggtt ggctggcctg gatctcagcc acaacctgct 350
caccagcatc tcacccactg cttctcccg cttcgctac ctggagtcgc 400

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<210> 397
<211> 353
<212> PRT
<213> Homo sapiens

<400> 397
Met Pro Trp Pro Leu Leu Leu Leu Ala Val Ser Gly Ala Gln
1 5 10 15
Thr Thr Arg Pro Cys Phe Pro Gly Cys Gln Cys Glu Val Glu Thr
20 25 30
Phe Gly Leu Phe Asp Ser Phe Ser Leu Thr Arg Val Asp Cys Ser
35 40 45
Gly Leu Gly Pro His Ile Met Pro Val Pro Ile Pro Leu Asp Thr
50 55 60
Ala His Leu Asp Leu Ser Ser Asn Arg Leu Glu Met Val Asn Glu
65 70 75
Ser Val Leu Ala Gly Pro Gly Tyr Thr Thr Leu Ala Gly Leu Asp
80 85 90

Leu	Ser	His	Asn	Leu	Leu	Thr	Ser	Ile	Ser	Pro	Thr	Ala	Phe	Ser
				95					100					105
Arg	Leu	Arg	Tyr	Leu	Glu	Ser	Leu	Asp	Leu	Ser	His	Asn	Gly	Leu
				110					115					120
Thr	Ala	Leu	Pro	Ala	Glu	Ser	Phe	Thr	Ser	Ser	Pro	Leu	Ser	Asp
				125					130					135
Val	Asn	Leu	Ser	His	Asn	Gln	Leu	Arg	Glu	Val	Ser	Val	Ser	Ala
				140					145					150
Phe	Thr	Thr	His	Ser	Gln	Gly	Arg	Ala	Leu	His	Val	Asp	Leu	Ser
				155					160					165
His	Asn	Leu	Ile	His	Arg	Leu	Val	Pro	His	Pro	Thr	Arg	Ala	Gly
				170					175					180
Leu	Pro	Ala	Pro	Thr	Ile	Gln	Ser	Leu	Asn	Leu	Ala	Trp	Asn	Arg
				185					190					195
Leu	His	Ala	Val	Pro	Asn	Leu	Arg	Asp	Leu	Pro	Leu	Arg	Tyr	Leu
				200					205					210
Ser	Leu	Asp	Gly	Asn	Pro	Leu	Ala	Val	Ile	Gly	Pro	Gly	Ala	Phe
				215					220					225
Ala	Gly	Leu	Gly	Gly	Leu	Thr	His	Leu	Ser	Leu	Ala	Ser	Leu	Gln
				230					235					240
Arg	Leu	Pro	Glu	Leu	Ala	Pro	Ser	Gly	Phe	Arg	Glu	Leu	Pro	Gly
				245					250					255
Leu	Gln	Val	Leu	Asp	Leu	Ser	Gly	Asn	Pro	Lys	Leu	Asn	Trp	Ala
				260					265					270
Gly	Ala	Glu	Val	Phe	Ser	Gly	Leu	Ser	Ser	Leu	Gln	Glu	Leu	Asp
				275					280					285
Leu	Ser	Gly	Thr	Asn	Leu	Val	Pro	Leu	Pro	Glu	Ala	Leu	Leu	Leu
				290					295					300
His	Leu	Pro	Ala	Leu	Gln	Ser	Val	Ser	Val	Gly	Gln	Asp	Val	Arg
				305					310					315
Cys	Arg	Arg	Leu	Val	Arg	Glu	Gly	Thr	Tyr	Pro	Arg	Arg	Pro	Gly
				320					325					330
Ser	Ser	Pro	Lys	Val	Pro	Leu	His	Cys	Val	Asp	Thr	Arg	Glu	Ser
				335					340					345
Ala	Ala	Arg	Gly	Pro	Thr	Ile	Leu							
				350										

<210> 398

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398
ccctgccagc cgagagcttc acc 23

<210> 399
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 399
ggttggtgcc cgaaagggtcc agc 23

<210> 400
<211> 44
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 400
caaccccaag cttaactggg caggagctga ggtgtttca ggcc 44

<210> 401
<211> 1571
<212> DNA
<213> Homo sapiens

<400> 401
gatggcgca ggcacagcttc tgtgagattc gatttctccc cagttcccc 50
gtgggtctga ggggaccaga agggtgagct acgttggctt tctgaaagg 100
gaggctatat gcgtcaattc cccaaaacaa gtttgacat ttccccctgaa 150
atgtcattct ctatctattc actgcaagtg cctgctgttc caggccttac 200
ctgctggca ctaacggcg agccaggatg gggacagaat aaaggagcca 250
cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300
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ctgcgtttta tctccttatgg actccttcca ctggactgaa gacactcaat 450
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gaatcttaag gaggactgag tctttcaag acacaaagcc tgcgaatcga 600
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gagtcacttt gaaaagctgg aacctcaggc agcagttgtg aaggctttgg 850
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atttttgtaa tatcttctg ctattggata tatttatttag ttaatataatt 1150
tatttatttt ttgctattta atgtattttt tttttactt ggacatgaaa 1200
ctttaaaaaaa attcacagat tatatttata acctgactag agcaggtgat 1250
gtatTTTtat acagtaaaaaa aaaaaaacct tgtaaattct agaagagtgg 1300
ctaggggggt tattcatttg tattcaacta aggacatatt tactcatgct 1350
gatgctctgt gagatatttg aaattgaacc aatgactact taggatgggt 1400
tgtggataa gtttgatgt ggaattgcac atctacctta caattactga 1450
ccatccccag tagactcccc agtcccataa ttgttatct tccagccagg 1500
aatcctacac ggccagcatg tatttctaca aataaagttt tctttgcata 1550
ccaaaaaaaaa aaaaaaaaaa a 1571

<210> 402
<211> 261
<212> PRT
<213> Homo sapiens

<400> 402
Met Arg Gln Phe Pro Lys Thr Ser Phe Asp Ile Ser Pro Glu Met
1 5 10 15
Ser Phe Ser Ile Tyr Ser Leu Gln Val Pro Ala Val Pro Gly Leu
20 25 30
Thr Cys Trp Ala Leu Thr Ala Glu Pro Gly Trp Gly Gln Asn Lys
35 40 45

Gly Ala Thr Thr Cys Ala Thr Asn Ser His Ser Asp Ser Glu Leu
50 55 60

Arg Pro Glu Ile Phe Ser Ser Arg Glu Ala Trp Gln Phe Phe Leu
65 70 75

Leu Leu Trp Ser Pro Asp Phe Arg Pro Lys Met Lys Ala Ser Ser
80 85 90

Leu Ala Phe Ser Leu Leu Ser Ala Ala Phe Tyr Leu Leu Trp Thr
95 100 105

Pro Ser Thr Gly Leu Lys Thr Leu Asn Leu Gly Ser Cys Val Ile
110 115 120

Ala Thr Asn Leu Gln Glu Ile Arg Asn Gly Phe Ser Glu Ile Arg
125 130 135

Gly Ser Val Gln Ala Lys Asp Gly Asn Ile Asp Ile Arg Ile Leu
140 145 150

Arg Arg Thr Glu Ser Leu Gln Asp Thr Lys Pro Ala Asn Arg Cys
155 160 165

Cys Leu Leu Arg His Leu Leu Arg Leu Tyr Leu Asp Arg Val Phe
170 175 180

Lys Asn Tyr Gln Thr Pro Asp His Tyr Thr Leu Arg Lys Ile Ser
185 190 195

Ser Leu Ala Asn Ser Phe Leu Thr Ile Lys Lys Asp Leu Arg Leu
200 205 210

Ser His Ala His Met Thr Cys His Cys Gly Glu Glu Ala Met Lys
215 220 225

Lys Tyr Ser Gln Ile Leu Ser His Phe Glu Lys Leu Glu Pro Gln
230 235 240

Ala Ala Val Val Lys Ala Leu Gly Glu Leu Asp Ile Leu Leu Gln
245 250 255

Trp Met Glu Glu Thr Glu
260

<210> 403
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 403
ctcctgtggc ctccagattt caggccta 28

<210> 404
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 404
agtccctcctt aagattctga tgtcaa 26

<210> 405
<211> 998
<212> DNA
<213> Homo sapiens

<400> 405
ccgttatcgt cttgcgctac tgctgaatgt ccgtccccga ggaggaggag 50
aggctttgc cgctgaccca gagatggccc cgagcgagca aattcctact 100
gtccggctgc gcggctaccg tggccgagct agcaaccttt cccctggatc 150
tcacaaaaac tcgactccaa atgcaaggag aagcagctct tgctcggttg 200
ggagacggtg caagagaatc tgccccctat agggaatgg tgcgcacagc 250
cctagggatc attgaagagg aaggcttct aaagcttgg caaggagtga 300
cacccgccat ttacagacac gtagtgtatt ctggaggtcg aatggtcaca 350
tatgaacatc tccgagaggt tgggtttggc aaaagtgaag atgagcatta 400
tccccttgg aaatcagtca ttggagggat gatggctggt gttattggcc 450
agtttttagc caatccaact gacctagtga agttcagat gcaaatggaa 500
ggaaaaagga aactggaagg aaaaccattt cgatttcgtg gtgtacatca 550
tgcatttgca aaaatcttag ctgaaggagg aatacgaggg ctggggcag 600
gctgggtacc caatatacaa agagcagcac tggtaatat gggagattta 650
accacttatg atacagtcaa acactacttg gtattgaata caccacttga 700
ggacaatatc atgactcactg gtttatcaag tttatgttct ggactggtag 750
cttctattct gggAACACCA gccgatgtca tcaaaAGCAG aataatgaat 800
caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850
ctgcttgatt caggctgttc aaggtgaagg attcatgagt ctatataaag 900
gcttttacc atcttggctg agaatgaccc ctggtaat ggtgttctgg 950
cttacttatg aaaaaatcag agagatgagt ggagtcaat cattttaa 998

<210> 406
<211> 323
<212> PRT
<213> Homo sapiens

<400> 406

Met	Ser	Val	Pro	Glu	Glu	Glu	Glu	Arg	Leu	Leu	Pro	Leu	Thr	Gln
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Arg	Trp	Pro	Arg	Ala	Ser	Lys	Phe	Leu	Leu	Ser	Gly	Cys	Ala	Ala
				20				25					30	
Thr	Val	Ala	Glu	Leu	Ala	Thr	Phe	Pro	Leu	Asp	Leu	Thr	Lys	Thr
				35				40					45	
Arg	Leu	Gln	Met	Gln	Gly	Glu	Ala	Ala	Leu	Ala	Arg	Leu	Gly	Asp
			50				55					60		
Gly	Ala	Arg	Glu	Ser	Ala	Pro	Tyr	Arg	Gly	Met	Val	Arg	Thr	Ala
		65					70					75		
Leu	Gly	Ile	Ile	Glu	Glu	Glu	Gly	Phe	Leu	Lys	Leu	Trp	Gln	Gly
			80					85					90	
Val	Thr	Pro	Ala	Ile	Tyr	Arg	His	Val	Val	Tyr	Ser	Gly	Gly	Arg
			95				100					105		
Met	Val	Thr	Tyr	Glu	His	Leu	Arg	Glu	Val	Val	Phe	Gly	Lys	Ser
				110				115				120		
Glu	Asp	Glu	His	Tyr	Pro	Leu	Trp	Lys	Ser	Val	Ile	Gly	Gly	Met
			125					130				135		
Met	Ala	Gly	Val	Ile	Gly	Gln	Phe	Leu	Ala	Asn	Pro	Thr	Asp	Leu
			140					145				150		
Val	Lys	Val	Gln	Met	Gln	Met	Glu	Gly	Lys	Arg	Lys	Leu	Glu	Gly
			155				160					165		
Lys	Pro	Leu	Arg	Phe	Arg	Gly	Val	His	His	Ala	Phe	Ala	Lys	Ile
			170				175					180		
Leu	Ala	Glu	Gly	Ile	Arg	Gly	Leu	Trp	Ala	Gly	Trp	Val	Pro	
			185				190					195		
Asn	Ile	Gln	Arg	Ala	Ala	Leu	Val	Asn	Met	Gly	Asp	Leu	Thr	Thr
			200					205				210		
Tyr	Asp	Thr	Val	Lys	His	Tyr	Leu	Val	Leu	Asn	Thr	Pro	Leu	Glu
			215				220					225		
Asp	Asn	Ile	Met	Thr	His	Gly	Leu	Ser	Ser	Leu	Cys	Ser	Gly	Leu
			230					235				240		
Val	Ala	Ser	Ile	Leu	Gly	Thr	Pro	Ala	Asp	Val	Ile	Lys	Ser	Arg
			245				250					255		

Ile Met Asn Gln Pro Arg Asp Lys Gln Gly Arg Gly Leu Leu Tyr
260 265 270

Lys Ser Ser Thr Asp Cys Leu Ile Gln Ala Val Gln Gly Glu Gly
275 280 285

Phe Met Ser Leu Tyr Lys Gly Phe Leu Pro Ser Trp Leu Arg Met
290 295 300

Thr Pro Trp Ser Met Val Phe Trp Leu Thr Tyr Glu Lys Ile Arg
305 310 315

Glu Met Ser Gly Val Ser Pro Phe
320

<210> 407
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 407
cgccggatccc gttatcgtct tgcgctactg c 31

<210> 408
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 408
gcggaattct taaaatggac tgactccact catc 34

<210> 409
<211> 1487
<212> DNA
<213> Homo sapiens

<400> 409
cggacgcgtg ggccggggac gccggcaggg ttgtggcgca gcagtctcct 50
tcctgcgcgc ggcgcctgaag tcggcgtggg cgttttagga agctggata 100
cagcatttaa tgaaaaattt atgcttaaga agtaaaaatg gcaggctcc 150
tagataattt tcgttgccca gaatgtgaat gtattgactg gagtgagaga 200
agaaaatgctg tggcatctgt tgtcgcaggt atattgtttt ttacaggctg 250
gtggataatg attgatgcag ctgtggtgta tcctaagcca gaacagttga 300
accatgcctt tcacacatgt ggtgtatTTT ccacattggc tttcttcattg 350

ataaatgctg tatccaatgc tcaggtgaga ggtgatagct atgaaagcgg 400
ctgttagga agaacaggtg ctcgagtttgc ttttcatt gtttcatgt 450
tgatgttgg gtcacttatt gttccatgt ggattttt tggtcataat 500
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cataaaaggt ttctcagcaag ttgttaactta ttttggccta aaaatgaggt 1350
tttttggta aagaaaaat atttggctt atgtattgaa gaagtgtact 1400
tttatataat gatTTTAA atgccccaaag gactagtttgc aaagcttctt 1450
ttaaaaagaa ttccctcaat atgactttat gtgagaa 1487

<210> 410
<211> 158
<212> PRT
<213> Homo sapiens

<400> 410
Met Ala Gly Phe Leu Asp Asn Phe Arg Trp Pro Glu Cys Glu Cys
1 5 10 15
Ile Asp Trp Ser Glu Arg Arg Asn Ala Val Ala Ser Val Val Ala
20 25 30

Gly Ile Leu Phe Phe Thr Gly Trp Trp Ile Met Ile Asp Ala Ala
35 40 45

Val Val Tyr Pro Lys Pro Glu Gln Leu Asn His Ala Phe His Thr
50 55 60

Cys Gly Val Phe Ser Thr Leu Ala Phe Phe Met Ile Asn Ala Val
65 70 75

Ser Asn Ala Gln Val Arg Gly Asp Ser Tyr Glu Ser Gly Cys Leu
80 85 90

Gly Arg Thr Gly Ala Arg Val Trp Leu Phe Ile Gly Phe Met Leu
95 100 105

Met Phe Gly Ser Leu Ile Ala Ser Met Trp Ile Leu Phe Gly Ala
110 115 120

Tyr Val Thr Gln Asn Thr Asp Val Tyr Pro Gly Leu Ala Val Phe
125 130 135

Phe Gln Asn Ala Leu Ile Phe Phe Ser Thr Leu Ile Tyr Lys Phe
140 145 150

Gly Arg Thr Glu Glu Leu Trp Thr
155

<210> 411
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 411
gttgaggaa gctgggatac 20

<210> 412
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 412
ccaaactcga gcacctgttc 20

<210> 413
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 413
atggcaggct tcctagataa tttcggttgg ccagaatgtg 40

<210> 414
<211> 1337
<212> DNA
<213> Homo sapiens

<400> 414
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gcagctggcc cactggcgcc ccgcaacact ccgtctcacc ctctgggcc 100
actgcacatcta gaggagggcc gtctgtgagg ccactacccc tccagcaact 150
gggaggtggg actgtcagaa gctggcccag ggtgggtgc agctgggtca 200
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aagtgggagc ctcgagccct cgggtggaag ctgaccccaa gccacccttc 300
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cataaaaacc atccgtctgc cacgctggct ggcagcctcg cccaccaagg 450
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aactactttg cgtttaaat ctgcagtggg gcccacaacg tcgtgggcc 550
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ctggcacaga aggcatttga catgtactct ggagatgtt agcacccatgt 700
gaaattcctt aaagaaattc cgggggggtgc actgggtctg gtggcctcct 750
acgacgatcc agggaccaaa atgaacgatg aaagcagggaa actttctct 800
gacttgggga gttcctacgc aaaacaactg ggcttccggg acagctgggt 850
cttcatacgaa gccaagacc tcaggggtaa aagcccttt gagcagttct 900
taaagaacag cccagacaca aacaaatacg agggatggcc agagctgctg 950
gagatggagg gctgcacgcc cccgaagcca ttttagggtg gctgtggctc 1000
ttcctcagcc aggggcctga agaagctcct gcctgactta ggagtcagag 1050
cccgccaggg gctgaggagg aggagcaggg ggtgctgcgt ggaaggtgt 1100
gcaggtcctt gcacgctgtg tcgcgcctct cctcctcgga aacagaaccc 1150
tcccacagca catcctaccc ggaagaccag cctcagaggg tccttctgga 1200

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accagctgtc tgtggagaga atggggtgct ttcgtcagg actgctgacg 1250  
gctggtcctg aggaaggaca aactgcccag acttgagccc aattaaattt 1300  
tatttttqct qtttttqaaa aaaaaaaaaa aaaaaaaaa 1337
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<210> 415
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<213> *Homo sapiens*

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 Met Arg Val Ser Gly Val Leu Arg Leu Leu Ala Leu Ile Phe Ala
 1 5 10 15
 Ile Val Thr Thr Trp Met Phe Ile Arg Ser Tyr Met Ser Phe Ser
 20 25 30
 Met Lys Thr Ile Arg Leu Pro Arg Trp Leu Ala Ala Ser Pro Thr
 35 40 45
 Lys Glu Ile Gln Val Lys Lys Tyr Lys Cys Gly Leu Ile Lys Pro
 50 55 60
 Cys Pro Ala Asn Tyr Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala
 65 70 75
 Asn Val Val Gly Pro Thr Met Cys Phe Glu Asp Arg Met Ile Met
 80 85 90
 Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu
 95 100 105
 Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp
 110 115 120
 Met Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu
 125 130 135
 Ile Pro Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro
 140 145 150
 Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu
 155 160 165
 Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val
 170 175 180
 Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln
 185 190 195
 Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro
 200 205 210
 Glu Leu Leu Glu Met Glu Gly Cys Met Pro Pro Lys Pro Phe
 215 220

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<220>
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<210> 417
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<220>
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<400> 417
ggatggccag agctgctg 18

<210> 418
<211> 26
<212> DNA
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<220>
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<400> 418
aaagtacaag tgtggcctca tcaaggc 26

<210> 419
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<220>
<223> Synthetic oligonucleotide probe

<400> 419
tctgactcct aagtcaaggca ggag 24

<210> 420
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<212> DNA
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<220>
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<400> 420
attctctcca cagacagctg gttc 24

<210> 421

<211> 46
<212> DNA
<213> Artificial Sequence

<220>
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<400> 421
gtacaagtgt ggcctcatca agccctgcc agccaactac tttgcg 46

<210> 422
<211> 1701
<212> DNA
<213> Homo sapiens

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<221> unsure
<222> 1528
<223> unknown base

<400> 422
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cacgccagga gctcgctcgc tctctctctc tctctctcac tcctccctcc 200
ctctctctct gcctgtccta gtcctctagt cctcaaattc ccagtcccct 250
gcaccccttc ctgggacact atgttgttct ccgcctcct gctggaggtg 300
atttggatcc tggctgcaga tgggggtcaa cactggacgt atgagggccc 350
acatggtcag gaccattggc cagcctctta ccctgagtgt ggaaacaatg 400
cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgaccctgat 450
ttgcctgctc tgcagccccca cggatatgac cagcctggca ccgagcctt 500
ggacctgcac aacaatggcc acacagtgca actctctctg ccctctaccc 550
tgtatctggg tggacttccc cgaaaatatg tagctgccccca gctccacctg 600
cactggggtc agaaaggatc cccaggggggg tcagaacacc agatcaacag 650
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atgacagctt gagtgaggct gctgagagggc ctcaggccct ggctgtcctg 750
ggcatcctaa ttgaggtggg tgagactaag aatatacgat atgaacacat 800
tctgagtcac ttgcataaag tcaggcataa agatcagaag acctcagtc 850
ctcccttcaa cctaagagag ctgctccccca aacagctggg gcagtacttc 900

cgctacaatg gctcgctcac aactccccct tgctaccaga gtgtgctctg 950
gacagtttt tatagaaggt cccagattc aatgaaacag ctggaaaagc 1000
ttcaggggac attgttctcc acagaagagg agccctctaa gcttctggta 1050
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cctcccccgt gacatctt agagaggaat ggaccaggc tgtcattcca 1450
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gaagtttggg atataccca aagtccctca cccctcaact tttatggccc 1600
tttccctaga tatactgcgg gatctctcct taggataaaag agttgctgtt 1650
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t 1701

<210> 423

<211> 337

<212> PRT

<213> Homo sapiens

<400> 423

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									20					30

Asp	His	Trp	Pro	Ala	Ser	Tyr	Pro	Glu	Cys	Gly	Asn	Asn	Ala	Gln
									35					45

Ser	Pro	Ile	Asp	Ile	Gln	Thr	Asp	Ser	Val	Thr	Phe	Asp	Pro	Asp
									50					60

Leu	Pro	Ala	Leu	Gln	Pro	His	Gly	Tyr	Asp	Gln	Pro	Gly	Thr	Glu
									65					75

Pro	Leu	Asp	Leu	His	Asn	Asn	Gly	His	Thr	Val	Gln	Leu	Ser	Leu
									80					90

Pro Ser Thr Leu Tyr Leu Gly Gly Leu Pro Arg Lys Tyr Val Ala
95 100 105

Ala Gln Leu His Leu His Trp Gly Gln Lys Gly Ser Pro Gly Gly
110 115 120

Ser Glu His Gln Ile Asn Ser Glu Ala Thr Phe Ala Glu Leu His
125 130 135

Ile Val His Tyr Asp Ser Asp Ser Tyr Asp Ser Leu Ser Glu Ala
140 145 150

Ala Glu Arg Pro Gln Gly Leu Ala Val Leu Gly Ile Leu Ile Glu
155 160 165

Val Gly Glu Thr Lys Asn Ile Ala Tyr Glu His Ile Leu Ser His
170 175 180

Leu His Glu Val Arg His Lys Asp Gln Lys Thr Ser Val Pro Pro
185 190 195

Phe Asn Leu Arg Glu Leu Leu Pro Lys Gln Leu Gly Gln Tyr Phe
200 205 210

Arg Tyr Asn Gly Ser Leu Thr Thr Pro Pro Cys Tyr Gln Ser Val
215 220 225

Leu Trp Thr Val Phe Tyr Arg Arg Ser Gln Ile Ser Met Glu Gln
230 235 240

Leu Glu Lys Leu Gln Gly Thr Leu Phe Ser Thr Glu Glu Glu Pro
245 250 255

Ser Lys Leu Leu Val Gln Asn Tyr Arg Ala Leu Gln Pro Leu Asn
260 265 270

Gln Arg Met Val Phe Ala Ser Phe Ile Gln Ala Gly Ser Ser Tyr
275 280 285

Thr Thr Gly Glu Met Leu Ser Leu Gly Val Gly Ile Leu Val Gly
290 295 300

Cys Leu Cys Leu Leu Ala Val Tyr Phe Ile Ala Arg Lys Ile
305 310 315

Arg Lys Lys Arg Leu Glu Asn Arg Lys Ser Val Val Phe Thr Ser
320 325 330

Ala Gln Ala Thr Thr Glu Ala
335

<210> 424

<211> 18

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<210> 425
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 425
cccgatctgc ctgctgta 18

<210> 426
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 426
ctgcactgta tggccattat tttt 24

<210> 427
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 427
cagaaaccca tgatacccta ctgaacacccg aatcccctgg aagcc 45

<210> 428
<211> 1073
<212> DNA
<213> Homo sapiens

<400> 428
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gattctactg ttttgttttc taggatcaac tcggcattt ccacagctca 150
aacctgcttt gggactccct cccacaaaac tggctccgga tcaggaaaca 200
ctaccaaacc aacagcagtc aaatcaggtc tttccttctt taagtctgat 250
accattaaca cagatgctca cactggggcc agatctgcat ctgttaaatc 300

ctgctgcagg aatgacacct ggtacccaga cccaccatt gaccctggga 350
gggttgaatg tacaacagca actgcaccca catgtgttac caattttgt 400
cacacaactt ggagcccagg gcactatcct aagctcagag gaattgccac 450
aaatcttcac gagcctcatc atccattcct tgcccggg aggcattcctg 500
cccaccagtc aggaggggc taatccagat gtccaggatg gaagccttcc 550
agcaggagga gcaggtgtaa atcctgccac ccagggAACCC ccagcaggcc 600
gcctcccaac tcccagtggc acagatgacg actttgcagt gaccaccct 650
gcaggcatcc aaaggagcac acatgccatc gaggaagcca ccacagaatc 700
agcaaatgga attcagtaag ctgtttcaaa tttttcaac taagctgcct 750
cgaattttgt gatacatgtg aatctttatc attgattata ttatggaata 800
gattgagaca cattggatag tcttagaaga aattaattct taatttacct 850
gaaaatattc ttgaaatttc agaaaatatg ttctatgttag agaatccaa 900
ctttaaaaaa caataattca atggataaat ctgtcttga aatataacat 950
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1050
aaaaaaaaaa aaaaaaaaaa aaa 1073

<210> 429
<211> 209
<212> PRT
<213> Homo sapiens

<400> 429
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20 25 30
Leu Ala Pro Asp Gln Gly Thr Leu Pro Asn Gln Gln Ser Asn
35 40 45
Gln Val Phe Pro Ser Leu Ser Leu Ile Pro Leu Thr Gln Met Leu
50 55 60
Thr Leu Gly Pro Asp Leu His Leu Leu Asn Pro Ala Ala Gly Met
65 70 75
Thr Pro Gly Thr Gln Thr His Pro Leu Thr Leu Gly Gly Leu Asn
80 85 90
Val Gln Gln Gln Leu His Pro His Val Leu Pro Ile Phe Val Thr

	95	100	105											
Gln	Leu	Gly	Ala	Gln	Gly	Thr	Ile	Leu	Ser	Ser	Glu	Glu	Leu	Pro
				110				115					120	
Gln	Ile	Phe	Thr	Ser	Leu	Ile	Ile	His	Ser	Leu	Phe	Pro	Gly	Gly
				125				130					135	
Ile	Leu	Pro	Thr	Ser	Gln	Ala	Gly	Ala	Asn	Pro	Asp	Val	Gln	Asp
				140				145					150	
Gly	Ser	Leu	Pro	Ala	Gly	Gly	Ala	Gly	Val	Asn	Pro	Ala	Thr	Gln
				155				160					165	
Gly	Thr	Pro	Ala	Gly	Arg	Leu	Pro	Thr	Pro	Ser	Gly	Thr	Asp	Asp
				170				175					180	
Asp	Phe	Ala	Val	Thr	Thr	Pro	Ala	Gly	Ile	Gln	Arg	Ser	Thr	His
				185				190					195	
Ala	Ile	Glu	Glu	Ala	Thr	Thr	Glu	Ser	Ala	Asn	Gly	Ile	Gln	
				200				205						

<210> 430
<211> 1257
<212> DNA
<213> Homo Sapien

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cggagcgcgg cggagccaga cgctgaccac gttcctctcc tcggtctcct 100
ccgcctccag ctccgcgctg cccggcagcc gggagccatg cgaccccagg 150
cccccgccgc ctccccgcag cggctccgcg gcctcctgct gtcctgctg 200
ctgcagctgc ccgcgcgctc gagcgctct gagatcccc agggaaagca 250
aaaggcgca gtcggcaga gggaggtggt ggacctgtat aatggaatgt 300
gcttacaagg gccagcagga gtgcctggtc gagacggag ccctggggcc 350
aatgttattc cgggtacacc tggatccca ggtcggatg gattcaaagg 400
agaaaagggg gaatgtctga gggaaagctt tgaggagtcc tggacaccca 450
actacaagca gtgttcatgg agttcattga attatggcat agatcttggg 500
aaaattgcgg agtgtacatt tacaaagatg cgttcaaata gtgctctaag 550
agttttgttc agtggctcac ttccggctaaa atgcagaaat gcatgctgtc 600
agcgttggta tttcacattc aatggagctg aatgttcagg acctcttccc 650
attgaagcta taatttattt ggaccaagga agccctgaaa tgaattcaac 700

aattaatatt catcgactt cttctgtgga aggactttgt gaaggaattg 750
gtgctggatt agtggatgtt gctatctggg ttggcacttg ttcagattac 800
ccaaaaggag atgcttctac tggatgaaat tcagttctc gcatcattat 850
tgaagaacta ccaaaataaa tgcttaatt ttcatttgct acctctttt 900
ttattatgcc ttgaaatggt tcacttaat gacattttaa ataagtttat 950
gtatacatct gaatgaaaag caaagctaaa tatgttaca gaccaaagtg 1000
tgatttcaca ctgttttaa atcttagcatt attcatttg cttcaatcaa 1050
aagtggtttc aatattttt ttagttgggtt agaatacttt cttcatagtc 1100
acattctctc aacctataat ttgaaatatt gttgtggct tttgttttt 1150
ctcttagtat agcattttta aaaaaatata aaagctacca atctttgtac 1200
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tccaaca 1257

<210> 431
<211> 243
<212> PRT
<213> Homo Sapien

<400> 431

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Leu	Gln	Leu	Pro	Ala	Pro	Ser	Ser	Ala						
					20				25			30		
Ser	Glu	Ile	Pro	Lys	Gly	Lys	Gln	Lys	Ala	Gln	Leu	Arg	Gln	Arg
				35				40				45		
Glu	Val	Val	Asp	Leu	Tyr	Asn	Gly	Met	Cys	Leu	Gln	Gly	Pro	Ala
				50				55				60		
Gly	Val	Pro	Gly	Arg	Asp	Gly	Ser	Pro	Gly	Ala	Asn	Val	Ile	Pro
				65				70				75		
Gly	Thr	Pro	Gly	Ile	Pro	Gly	Arg	Asp	Gly	Phe	Lys	Gly	Glu	Lys
				80				85				90		
Gly	Glu	Cys	Leu	Arg	Glu	Ser	Phe	Glu	Glu	Ser	Trp	Thr	Pro	Asn
				95				100				105		
Tyr	Lys	Gln	Cys	Ser	Trp	Ser	Ser	Leu	Asn	Tyr	Gly	Ile	Asp	Leu
				110				115				120		
Gly	Lys	Ile	Ala	Glu	Cys	Thr	Phe	Thr	Lys	Met	Arg	Ser	Asn	Ser
				125				130				135		

Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg
140 145 150

Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu
155 160 165

Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln
170 175 180

Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser
185 190 195

Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp
200 205 210

Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp
215 220 225

Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu
230 235 240

Leu Pro Lys

<210> 432
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<212> DNA
<213> Artificial Sequence

<220>
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<400> 432
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<210> 433
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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cgcaggacag ttgtgaaaat a 21

<210> 434
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 434
atgacgctcg tccaaggcca c 21

<210> 435
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<212> DNA
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<220>
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<400> 435
cccacctgta ccaccatgt 19

<210> 436
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<220>
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<400> 436
actccaggca ccatctgttc tccc 24

<210> 437
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<220>
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<400> 437
aagggctggc attcaagtc 19

<210> 438
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<213> Artificial Sequence

<220>
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<400> 438
tgacctggca aaggaagaa 19

<210> 439
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<220>
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<400> 439
cagccaccct ccagtccaag g 21

<210> 440
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<212> DNA
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<220>
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<400> 440
gggtcggtt ttggagaga 19

<210> 441
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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<400> 441
ctggccctca gagcaccaat 20

<210> 442
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<220>
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<400> 442
tcctccatca cttcccctag ctcca 25

<210> 443
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 443
ctggcaggag ttaaaagttcc aaga 24

<210> 444
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 444
aaaggacacc gggatgtg 18

<210> 445
<211> 26
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<220>
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<400> 445
agcgtacact ctctccaggc aaccag 26

<210> 446
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<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 446
caattctgga tgaggtggta ga 22

<210> 447
<211> 20
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<220>
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<400> 447
caggactgag cgcttggta 20

<210> 448
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<220>
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<400> 448
caaagcgcca agtaccggac c 21

<210> 449
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
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<400> 449
ccagacctca gccaggaa 18

<210> 450
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 450
cccttagctga ccccttca 18

<210> 451
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 451
tctgacaaggc agttttctga atc 23

<210> 452
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 452
ctctccccct ccctttcct ttgttt 26

<210> 453
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 453
ctctggtgcc cacagtga 18

<210> 454
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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ccatgcctgc tcagccaaga a 21

<210> 455
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 455
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<210> 456
<211> 20
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ccttgaaaag gaccaggatt 20

<210> 457
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<212> DNA
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<220>
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<400> 457
atgagtcgca cctgctgttc cc 22

<210> 458
<211> 18
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<220>
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<400> 458
tagcagctgc cttggta 18

<210> 459
<211> 22
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 459
aacagcaggt gcgactcatc ta 22

<210> 460
<211> 23
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<220>
<223> Synthetic oligonucleotide probe

<400> 460
tgcttaggcga cgacacccag acc 23

<210> 461
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<212> DNA
<213> Artificial Sequence

<220>
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<400> 461
tggacacgtg gcagtgga 18

<210> 462
<211> 19
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<220>
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<400> 462
tcatggtctc gtcccattc 19

<210> 463
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<212> DNA
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<400> 463
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<210> 464
<211> 18
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<400> 464
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<210> 465
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<400> 465
tccccattag cacaggagta 20

<210> 466

<211> 23
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<220>
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aggctttgc ctgtcctgct gct 23

<210> 467
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<220>
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<400> 467
gcccgagatc ccacttgt 18

<210> 468
<211> 19
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<213> Artificial Sequence

<220>
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<400> 468
actgctccgc ctactacga 19

<210> 469
<211> 20
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<220>
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<210> 470
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<400> 470
aaggccaagg tgagtccat 19

<210> 471
<211> 20
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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 471
cgagtgttg cgaaacctaa 20

<210> 472
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 472
tcagggtcta catcagcctc ctgc 24

<210> 473
<211> 19
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 473
aaggccaagg tgagtccat 19

<210> 474
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 474
cctactgagg agccctatgc 20

<210> 475
<211> 22
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 475
tccaggtgga ccccacttca gg 22

<210> 476
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 476

gggaggctta taggccaaat ctgg 24

<210> 477

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 477

ggcttcagca gcacgtgtga agtcgaagtgc cagtcacag atatcaatga 50

-230-

-1-

Val Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala
20 25 30

Gly Ile Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu
35 40 45

Pro Asp Ile Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn
50 55 60

Leu His Glu Arg Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg
65 70 75

Arg Leu Val Val Ser Leu Gly Thr Val Asp Val Leu Lys Gin His
80 85 90

Ile Asn Pro Asn Lys Thr Ser Asp Pro Phe Glu Thr Met Leu Lys
95 100 105

Ser Leu Leu Arg Tyr Gln Ser Gly Gly Ser Val Ser Glu Asn
110 115 120

His Met Arg Lys Lys Leu Tyr Glu Asn Gly Val Thr Asp Ser Leu
125 130 135

Lys Ser Asn Phe Ala Leu Leu Leu Lys Leu Ser Glu Glu Leu Leu
140 145 150

Asp Lys Trp Leu Ser Tyr Pro Glu Thr Gln His Val Pro Leu Ser
155 160 165

Gln His Met Leu Gly Phe Ala Met Lys Ser Val Thr Gln Met Val
170 175 180

Met Gly Ser Thr Phe Glu Asp Asp Gln Glu Val Ile Arg Phe Gln
185 190 195

Lys Asn His Gly Thr Val Trp Ser Glu Ile Gly Lys Gly Phe Leu
200 205 210

Asp Gly Ser Leu Asp Lys Asn Met Thr Arg Lys Lys Gln Tyr Glu
215 220 225

Asp Ala Leu Met Gln Leu Glu Ser Val Leu Arg Asn Ile Ile Lys
230 235 240

Glu Arg Lys Gly Arg Asn Phe Ser Gln His Ile Phe Ile Asp Ser
245 250 255

Leu Val Gln Gly Asn Leu Asn Asp Gln Gln Ile Leu Glu Asp Ser
260 265 270

Met Ile Phe Ser Leu Ala Ser Cys Ile Ile Thr Ala Lys Leu Cys
275 280 285

Thr Trp Ala Ile Cys Phe Leu Thr Thr Ser Glu Glu Val Gln Lys
290 295 300

Lys	Leu	Tyr	Glu	Glu	Ile	Asn	Gln	Val	Phe	Gly	Asn	Gly	Pro	Val
					305			310					315	
Thr	Pro	Glu	Lys	Ile	Glu	Gln	Leu	Arg	Tyr	Cys	Gln	His	Val	Leu
					320			325					330	
Cys	Glu	Thr	Val	Arg	Thr	Ala	Lys	Leu	Thr	Pro	Val	Ser	Ala	Gln
					335			340					345	
Leu	Gln	Asp	Ile	Glu	Gly	Lys	Ile	Asp	Arg	Phe	Ile	Ile	Pro	Arg
					350			355					360	
Glu	Thr	Leu	Val	Leu	Tyr	Ala	Leu	Gly	Val	Val	Leu	Gln	Asp	Pro
					365			370					375	
Asn	Thr	Trp	Pro	Ser	Pro	His	Lys	Phe	Asp	Pro	Asp	Arg	Phe	Asp
					380			385					390	
Asp	Glu	Leu	Val	Met	Lys	Thr	Phe	Ser	Ser	Leu	Gly	Phe	Ser	Gly
					395			400					405	
Thr	Gln	Glu	Cys	Pro	Glu	Leu	Arg	Phe	Ala	Tyr	Met	Val	Thr	Thr
					410			415					420	
Val	Leu	Leu	Ser	Val	Leu	Val	Lys	Arg	Leu	His	Leu	Leu	Ser	Val
					425			430					435	
Glu	Gly	Gln	Val	Ile	Glu	Thr	Lys	Tyr	Glu	Leu	Val	Thr	Ser	Ser
					440			445					450	
Arg	Glu	Glu	Ala	Trp	Ile	Thr	Val	Ser	Lys	Arg	Tyr			
					455			460						

<210> 213
<211> 759
<212> DNA
<213> Homo sapiens

<400> 213
ctagatttgt cggcttgcgg ggagacttca ggagtcgctg tctctgaact 50
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tcagggcttg tgccctctcg ctccctgacg ctcctggcgc atctggtggt 150
cgtcatcacc ttattctggc cccgggacag caacatacag gcctgcctgc 200
ctctcacgtt cacccccgag gagtatgaca agcaggacat tcagctggtg 250
gccgcgcgtct ctgtcacccct gggcctttt gcagtgagc tggccggttt 300
cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350
gggctcactg tagtgcattcc gtggccctgt ctttctcat attcgagcgt 400
tgggagtgca ctacgtattt gtacatttt gtcttctgca gtgcccttcc 450

agctgtcact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga 500
aacccttctg attaccttca tgacggAAC ctaaggacga agcctacagg 550
ggcaaggGCC gcttcgtatt cctggaaAGA ggaaggcata ggcttcggtt 600
ttccccctcgG aaactgcttc tgctggagGA tatgtgttgg aataattacg 650
tcttgagtct gggattatcc gcattgtatt tagtgcttg taataaaaATA 700
tgtttttagG taacattaAG acttatatac agtttttagGG gacaattaaa 750
aaaaaaaa 759

<210> 214
<211> 140
<212> PRT
<213> Homo sapiens

<400> 214
Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe .Leu Thr Leu
1 5 10 15
Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp
20 25 30
Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu
35 40 45
Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr
50 55 60
Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val
65 70 75
Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His
80 85 90
Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp
95 100 105
Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu
110 115 120
Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu
125 130 135
Lys Lys Lys Pro Phe
140

<210> 215
<211> 697
<212> DNA
<213> Homo sapiens

<400> 215
tcccgacCC tgccgcctG ccactatgTC ccggcgcTCT atgctgcttG 50

cctgggctct ccccagcctc ctgcactcg gagcggctca ggagacagaa 100
gaccggcct gctgcagccc catagtgcccg cggAACGAGT ggaaggccct 150
ggcatcagag tgcggccagc acctgagcct gcccttacgc tatgtggtgg 200
tatgcacac ggcgggcagc agctgcaaca ccccccctc gtgccagcag 250
caggccccga atgtgcagca ctaccacatg aagacactgg gctggtgcg 300
cgtggctac aacttcctga ttggagaaga cgggctcgta tacgagggcc 350
gtggctggaa cttcacgggt gcccactca gtcacttatg gaaccccatg 400
tccattggca tcagcttcat gggcaactac atggatcggg tgcccacacc 450
ccaggccatc cgggcagccc agggtctact gcctgcggt gtggctcagg 500
gagccctgag gtccaaactat gtgctcaaag gacaccgggaa tgtgcagcgt 550
acactctctc caggcaacca gctctaccac ctcatccaga attggccaca 600
ctaccgctcc ccctgaggcc ctgctgatcc gcacccatt cctccctcc 650
catggccaaa aacccactg tctccttctc caataaagat gtagctc 697

<210> 216
<211> 196
<212> PRT
<213> Homo sapiens

<400> 216
Met Ser Arg Arg Ser Met Leu Leu Ala Trp Ala Leu Pro Ser Leu
1 5 10 15
Leu Arg Leu Gly Ala Ala Gln Glu Thr Glu Asp Pro Ala Cys Cys
20 25 30
Ser Pro Ile Val Pro Arg Asn Glu Trp Lys Ala Leu Ala Ser Glu
35 40 45
Cys Ala Gln His Leu Ser Leu Pro Leu Arg Tyr Val Val Val Ser
50 55 60
His Thr Ala Gly Ser Ser Cys Asn Thr Pro Ala Ser Cys Gln Gln
65 70 75
Gln Ala Arg Asn Val Gln His Tyr His Met Lys Thr Leu Gly Trp
80 85 90
Cys Asp Val Gly Tyr Asn Phe Leu Ile Gly Glu Asp Gly Leu Val
95 100 105
Tyr Glu Gly Arg Gly Trp Asn Phe Thr Gly Ala His Ser Gly His
110 115 120

Leu	Trp	Asn	Pro	Met	Ser	Ile	Gly	Ile	Ser	Phe	Met	Gly	Asn	Tyr
				125					130					135
Met	Asp	Arg	Val	Pro	Thr	Pro	Gln	Ala	Ile	Arg	Ala	Ala	Gln	Gly
				140					145					150
Leu	Leu	Ala	Cys	Gly	Val	Ala	Gln	Gly	Ala	Leu	Arg	Ser	Asn	Tyr
				155					160					165
Val	Leu	Lys	Gly	His	Arg	Asp	Val	Gln	Arg	Thr	Leu	Ser	Pro	Gly
				170					175					180
Asn	Gln	Leu	Tyr	His	Leu	Ile	Gln	Asn	Trp	Pro	His	Tyr	Arg	Ser
				185					190					195

Pro

<210> 217
<211> 1871
<212> DNA
<213> Homo sapiens

<400> 217
ctgggacccc gaaaagagaa ggggagagcg aggggacgag agcggaggag 50
gaagatgcaa ctgactcgct gctgcttcgt gttcctgggt cagggttagcc 100
tctatctggc catctgtggc caggatgatg gtcctccgg ctcagaggac 150
cctgagcgtg atgaccacga gggccagccc cgccccggg tgcctcgaa 200
gcggggccac atctcaccta agtcccggcc catggccaat tccactctcc 250
tagggctgct ggccccgcct ggggaggctt gggcattct tgggcagccc 300
cccaaccgccc cgaaccacag ccccccaccc tcagccaagg tgaagaaaat 350
ctttggctgg ggcgacttct actccaaacat caagacggtg gccctgaacc 400
tgctcgtcac aggaaagatt gtggaccatg gcaatggac cttcagcgtc 450
cacttccaaac acaatgccac aggccagggaa aacatctcca tcagcctcg 500
gcggggcgt aaagctgttag agttccacca ggaacacgac atcttcatcg 550
aagccaaggc ctccaaaatc ttcaactgcc ggatggagtg ggagaaggta 600
gaacggggcc gccggaccc tcgttgcacc cacgacccag ccaagatctg 650
ctcccgagac cacgctcaga gctcagccac ctggagctgc tcccagccct 700
tcaaagtctgtcgt atcgccttct acagcacgga ctatcggtc 750
gtccagaagg tgtgcccaga ttacaactac catagtgata ccccctacta 800
cccatctggg tgaccgggg caggccacag aggccaggcc agggctggaa 850

ggacaggcct gcccattgcag gagaccatct ggacaccggg cagggaaagg 900
gttgggcctc aggccaggag ggggggtggag acgaggagat gccaagtggg 950
gccaggggca agtctcaagt ggcagagaaa gggtcccaag tgctggtccc 1000
aacctgaagc tgtggagtga cttagatcaca ggagcactgg aggaggagt 1050
ggctctctgt gcagcctcac agggcttgc cacggagcca cagagagatg 1100
ctgggtcccc gaggcctgtg ggcaggccga tcagtgtggc cccagatcaa 1150
gtcatggag gaagctaagc ctttggttct tgccatcctg aggaaagata 1200
gcaacaggga gggggagatt tcatcagtgt ggacagcctg tcaacttagg 1250
atggatggct gagagggctt cctaggagcc agtcagcagg gtgggtggg 1300
gccagaggag ctctccagcc ctgccttagtg ggccgcctga gccccttgc 1350
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gtcttgacag attgaccatc tgtctccagc caggccaccc ctttccaaaa 1450
ttccctttc tgccagtaact cccctgtac cacccattgc tcatggcaca 1500
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ctcctctggg agcatccatg tcccggagag gggtccctca acagtcagcc 1650
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tgttctgtgt gtctgtctgt ggggtgggggg aggggaggga agtcttgta 1800
aaccgctgat tgctgacttt tgtgtgaaga atcgtgttct tggagcagga 1850
aataaagctt gccccggggc a 1871

<210> 218

<211> 252

<212> PRT

<213> Homo sapiens

<400> 218

Met	Gln	Leu	Thr	Arg	Cys	Cys	Phe	Val	Phe	Leu	Val	Gln	Gly	Ser
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Leu	Tyr	Leu	Val	Ile	Cys	Gly	Gln	Asp	Asp	Gly	Pro	Pro	Gly	Ser
				20				25						30

Glu	Asp	Pro	Glu	Arg	Asp	Asp	His	Glu	Gly	Gln	Pro	Arg	Pro	Arg
			35					40						45

Val	Pro	Arg	Lys	Arg	Gly	His	Ile	Ser	Pro	Lys	Ser	Arg	Pro	Met
							50			55				60
Ala	Asn	Ser	Thr	Leu	Leu	Gly	Leu	Leu	Ala	Pro	Pro	Gly	Glu	Ala
							65			70				75
Trp	Gly	Ile	Leu	Gly	Gln	Pro	Pro	Asn	Arg	Pro	Asn	His	Ser	Pro
							80			85				90
Pro	Pro	Ser	Ala	Lys	Val	Lys	Lys	Ile	Phe	Gly	Trp	Gly	Asp	Phe
							95			100				105
Tyr	Ser	Asn	Ile	Lys	Thr	Val	Ala	Leu	Asn	Leu	Leu	Val	Thr	Gly
							110			115				120
Lys	Ile	Val	Asp	His	Gly	Asn	Gly	Thr	Phe	Ser	Val	His	Phe	Gln
							125			130				135
His	Asn	Ala	Thr	Gly	Gln	Gly	Asn	Ile	Ser	Ile	Ser	Leu	Val	Pro
							140			145				150
Pro	Ser	Lys	Ala	Val	Glu	Phe	His	Gln	Glu	Gln	Gln	Ile	Phe	Ile
							155			160				165
Glu	Ala	Lys	Ala	Ser	Lys	Ile	Phe	Asn	Cys	Arg	Met	Glu	Trp	Glu
							170			175				180
Lys	Val	Glu	Arg	Gly	Arg	Arg	Thr	Ser	Leu	Cys	Thr	His	Asp	Pro
							185			190				195
Ala	Lys	Ile	Cys	Ser	Arg	Asp	His	Ala	Gln	Ser	Ser	Ala	Thr	Trp
							200			205				210
Ser	Cys	Ser	Gln	Pro	Phe	Lys	Val	Val	Cys	Val	Tyr	Ile	Ala	Phe
							215			220				225
Tyr	Ser	Thr	Asp	Tyr	Arg	Leu	Val	Gln	Lys	Val	Cys	Pro	Asp	Tyr
							230			235				240
Asn	Tyr	His	Ser	Asp	Thr	Pro	Tyr	Tyr	Pro	Ser	Gly			
							245			250				

<210> 219

<211> 2065

<212> DNA

<213> Homo sapiens

<400> 219

gtgaatgtga gggtttgcgt actttcagat gtcttaggaac cagagtgggt 50

gcagggggccc caggcagggc tgattcttgg gcggaggaga gtagggtaaa 100

gggttctgca ttagctccctt aaaggacaaa ggtaacagag ccagcgagag 150

agctcgaggg gagactttga cttaagccca cagaatttgtt ggaagtgtgc 200

gcgcggccgc cgccgtcgct cctgcagcgc tgcgaccta gcccgttagca 250
tcttccccgag caccgggatc ccggggtagg aggcgacgct ggcgagcacc 300
agcgccagcc ggctgcggct gcccacacgg ctcaccatgg gctccggcgc 350
ccggcgctg tccgcggtgc cggccgtgct gctggcctc acgctgccgg 400
ggctgcccgt ctgggcacag aacgacacgg agcccatcggt gctggaggcgc 450
aagtgtctgg tggtgtgcga ctcgaacccg gccacggact ccaagggctc 500
ctcttcctcc ccgctgggaa tatcggtccg ggccggccaac tccaagggtcg 550
ccttctcgcc ggtgcggagc accaaccacg agccatccga gatgagcaac 600
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tttcacattt gagtctgtct ttgttagcacc aagaaaagga atttacagtt 700
tcagtttca cgtgattaaa gtctaccaga gccaaactat ccaggtaac 750
ttgatgttaa atggaaaacc agtaatatct gcctttgcgg gggacaaaga 800
tgttactcgt gaagctgcca cgaatgggtt cctgctctac ctagataaag 850
aggataaggt ttacctaaaa ctggagaaag gtaatttgggt tggaggctgg 900
cagtattcca cgtttctgg ctttctgggtt ttccccctat aggattcaat 950
ttctccatga tggtcatcca ggtgagggat gacccactcc ttagtttattt 1000
gaagatcatt ttttcatcat tggattgatg tcttttattt gtttctcatg 1050
ggtggatatg gattctaaagg attctagcct gtctgaacca atacaaaattt 1100
tcacagatta tttgtgtgt tctgtttcag tatatttggaa ttggggactct 1150
aagcagataa tacctatgct taaatgtaaac agtcaaaaagc tgtctgcaag 1200
acttattctg aatttcattt cctgggattt ctgaattttagt tacagatgtt 1250
gaattttattt tgtttagttt taaaagactg gcaaccaggt ctaaggattt 1300
gaaaactcta aagttctgac ttcaatcaac ggtagtgtt atactgccaa 1350
agaactgtat actgtgttaa tatattttagt atatttggttt ttattccttt 1400
ggaatttagtt tgtttggttc ttgtaaaaaaaaa cttggatttt tttttcagt 1450
aactggattt atgtttctc ttaaaaataag gtaatgaatg gcttgcccac 1500
aaatttacct tgactacgat atcatcgaca tgacttctct caaaaaaaaa 1550
gaatgcttca tagttgtatt ttaattgtat atgtgaaaga gtcataatttt 1600
ccaaaggataa ttttcttcaaga agaagaatag atcataaatac tgacaaggaa 1650

aaagttgctt acccaaaatc taagtgctca atccctgagc ctcagcaaaa 1700
cagctccctt ccgaggaaaa tcttatactt tattgctcaa cttaattaa 1750
aatgatttat aataaccact ttattaaaaa cctaaggaaa ttttttttc 1800
cgttagacatg accactttt taactggtgg tggatgctg ttgttctaa 1850
ttatacctat tttcaaggc ttctgttgta tttgaagtat catctggttt 1900
tgccttaact cttaatttg tatataattt tctgttagc taatattaaa 1950
ttcaaataatc ccatactaa atttagtgca atatcttgc tttgtatag 2000
gtcatatgaa ttcataaaat tattatgtc tgttatagaa taaagattaa 2050
tatatgtttaa aaaaa 2065

<210> 220

<211> 201

<212> PRT

<213> Homo sapiens

<400> 220

Met Gly Ser Gly Arg Arg Ala Leu Ser Ala Val Pro Ala Val Leu
1 5 10 15

Leu Val Leu Thr Leu Pro Gly Leu Pro Val Trp Ala Gln Asn Asp
20 25 30

Thr Glu Pro Ile Val Leu Glu Gly Lys Cys Leu Val Val Cys Asp
35 40 45

Ser Asn Pro Ala Thr Asp Ser Lys Gly Ser Ser Ser Pro Leu
50 55 60

Gly Ile Ser Val Arg Ala Ala Asn Ser Lys Val Ala Phe Ser Ala
65 70 75

Val Arg Ser Thr Asn His Glu Pro Ser Glu Met Ser Asn Lys Thr
80 85 90

Arg Ile Ile Tyr Phe Asp Gln Ile Leu Val Asn Val Gly Asn Phe
95 100 105

Phe Thr Leu Glu Ser Val Phe Val Ala Pro Arg Lys Gly Ile Tyr
110 115 120

Ser Phe Ser Phe His Val Ile Lys Val Tyr Gln Ser Gln Thr Ile
125 130 135

Gln Val Asn Leu Met Leu Asn Gly Lys Pro Val Ile Ser Ala Phe
140 145 150

Ala Gly Asp Lys Asp Val Thr Arg Glu Ala Ala Thr Asn Gly Val
155 160 165

Leu Leu Tyr Leu Asp Lys Glu Asp Lys Val Tyr Leu Lys Leu Glu
170 175 180

Lys Gly Asn Leu Val Gly Gly Trp Gln Tyr Ser Thr Phe Ser Gly
185 190 195

Phe Leu Val Phe Pro Leu
200

<210> 221
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 221
acggctcacc atgggctccg 20

<210> 222
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 222
aggaagagga gcccttggag tccg 24

<210> 223
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 223
cgtgctggag ggcaagtgtc tggtgggtgt cgactcgaac 40

<210> 224
<211> 902
<212> DNA
<213> Homo sapiens

<400> 224
cggtggccat gactgcggcc gtgttcttcg gctgcgcctt cattgccttc 50
gggcctgcgc tcgccctta tgtcttcacc atcgccatcg agccgttgcg 100
tatcatcttc ctcatcgccg gagctttctt ctgggtggtg tctctactga 150
tttcgtccct tgtttgggtc atggcaagag tcattattga caacaaagat 200

ggaccaacac agaaatatct gctgatctt ggagcgttt tctctgtcta 250
tatccaagaa atgttccgat ttgcataatta taaactctta aaaaaagcca 300
gtgaaggttt gaagagtata aaccaggta agacagcacc ctctatgcga 350
ctgctggcct atgtttctgg cttggcattt ggaatcatga gtggagtatt 400
ttcccttgtg aataccctat ctgactcattt gggccaggc acagtggca 450
ttcatggaga ttctcctcaa ttcttcctt attcagctt catgacgctg 500
gtcattatct tgctgcattt attctgggc attgtatattt ttgatggctg 550
tgagaagaaa aagtggggca tcctccttat cgtttcctg acccacctgc 600
tggtgtcagc ccagacccatc ataagttctt attatggaat aaacctggcg 650
tcagcattta taatcctggt gctcatggc acctggcat tcttagctgc 700
gggaggcagc tgccgaagcc tgaaactctg cctgctctgc caagacaaga 750
actttcttct ttacaaccag cgctccagat aacctcaggg aaccagcact 800
tcccaaaccg cagactacat cttagagga agcacaactg tgccttttc 850
tgaaaatccc ttttctggt ggaattgaga aagaaataaa actatgcaga 900
ta 902

<210> 225

<211> 257

<212> PRT

<213> Homo sapiens

<400> 225

Met	Thr	Ala	Ala	Val	Phe	Phe	Gly	Cys	Ala	Phe	Ile	Ala	Phe	Gly
1				5					10				15	

Pro	Ala	Leu	Ala	Leu	Tyr	Val	Phe	Thr	Ile	Ala	Ile	Glu	Pro	Leu
				20				25				30		

Arg	Ile	Ile	Phe	Leu	Ile	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser
				35				40				45		

Leu	Leu	Ile	Ser	Ser	Leu	Val	Trp	Phe	Met	Ala	Arg	Val	Ile	Ile
					50			55				60		

Asp	Asn	Lys	Asp	Gly	Pro	Thr	Gln	Lys	Tyr	Leu	Leu	Ile	Phe	Gly
				65				70				75		

Ala	Phe	Val	Ser	Val	Tyr	Ile	Gln	Glu	Met	Phe	Arg	Phe	Ala	Tyr
				80				85				90		

Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Ser	Glu	Gly	Leu	Lys	Ser	Ile	Asn
				95				100				105		

Pro Gly Glu Thr Ala Pro Ser Met Arg Leu Leu Ala Tyr Val Ser
110 115 120
Gly Leu Gly Phe Gly Ile Met Ser Gly Val Phe Ser Phe Val Asn
125 130 135
Thr Leu Ser Asp Ser Leu Gly Pro Gly Thr Val Gly Ile His Gly
140 145 150
Asp Ser Pro Gln Phe Phe Leu Tyr Ser Ala Phe Met Thr Leu Val
155 160 165
Ile Ile Leu Leu His Val Phe Trp Gly Ile Val Phe Phe Asp Gly
170 175 180
Cys Glu Lys Lys Lys Trp Gly Ile Leu Leu Ile Val Leu Leu Thr
185 190 195
His Leu Leu Val Ser Ala Gln Thr Phe Ile Ser Ser Tyr Tyr Gly
200 205 210
Ile Asn Leu Ala Ser Ala Phe Ile Ile Leu Val Leu Met Gly Thr
215 220 225
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Cys Leu Leu Cys Gln Asp Lys Asn Phe Leu Leu Tyr Asn Gln Arg
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Ser Arg

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<211> 3939
<212> DNA
<213> Homo sapiens

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<211> 832

<212> PRT

<213> Homo sapiens

<400> 227

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Lys Asp Ala Glu Phe Glu Arg Thr Tyr Val Asp Glu Val Asn Ser
35 40 45

Glu Leu Val Asn Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn
50 55 60

Arg Thr Glu Gly Val Arg Val Ser Val Asn Val Leu Asn Lys Gln
65 70 75

Lys Gly Ala Pro Leu Leu Phe Val Val Arg Gln Lys Glu Ala Val
80 85 90

Val Ser Phe Gln Val Pro Leu Ile Leu Arg Gly Met Phe Gln Arg
95 100 105

Lys Tyr Leu Tyr Gln Lys Val Glu Arg Thr Leu Cys Gln Pro Pro
110 115 120

Thr Lys Asn Glu Ser Glu Ile Gln Phe Phe Tyr Val Asp Val Ser

	125	130	135
Thr Leu Ser Pro Val Asn Thr Thr Tyr Gln Leu Arg Val Ser Arg			
140	145	150	
Met Asp Asp Phe Val Leu Arg Thr Gly Glu Gln Phe Ser Phe Asn			
155	160	165	
Thr Thr Ala Ala Gln Pro Gln Tyr Phe Lys Tyr Glu Phe Pro Glu			
170	175	180	
Gly Val Asp Ser Val Ile Val Lys Val Thr Ser Asn Lys Ala Phe			
185	190	195	
Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu Cys Pro Val Tyr			
200	205	210	
Asp Leu Asp Asn Asn Val Ala Phe Ile Gly Met Tyr Gln Thr Met			
215	220	225	
Thr Lys Lys Ala Ala Ile Thr Val Gln Arg Lys Asp Phe Pro Ser			
230	235	240	
Asn Ser Phe Tyr Val Val Val Val Lys Thr Glu Asp Gln Ala			
245	250	255	
Cys Gly Gly Ser Leu Pro Phe Tyr Pro Phe Ala Glu Asp Glu Pro			
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Val Asp Gln Gly His Arg Gln Lys Thr Leu Ser Val Leu Val Ser			
275	280	285	
Gln Ala Val Thr Ser Glu Ala Tyr Val Ser Gly Met Leu Phe Cys			
290	295	300	
Leu Gly Ile Phe Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu Ala			
305	310	315	
Cys Trp Glu Asn Trp Arg Gln Lys Lys Lys Thr Leu Leu Val Ala			
320	325	330	
Ile Asp Arg Ala Cys Pro Glu Ser Gly His Pro Arg Val Leu Ala			
335	340	345	
Asp Ser Phe Pro Gly Ser Ser Pro Tyr Glu Gly Tyr Asn Tyr Gly			
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Ser Phe Glu Asn Val Ser Gly Ser Thr Asp Gly Leu Val Asp Ser			
365	370	375	
Ala Gly Thr Gly Asp Leu Ser Tyr Gly Tyr Gln Gly Arg Ser Phe			
380	385	390	
Glu Pro Val Gly Thr Arg Pro Arg Val Asp Ser Met Ser Ser Val			
395	400	405	
Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp Lys			

410 415 420
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425 430 435
Arg Lys Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe
440 445 450
Trp Asn Ile Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val
455 460 465
Gln Leu Val Ile Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn
470 475 480
Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys Ala His Pro Leu Gly
485 490 495
Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu Gly Tyr Ile
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Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu Gln Arg Glu Ile
515 520 525
Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Cys Ala Leu Glu
530 535 540
Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr
545 550 555
Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr His Val Cys
560 565 570
Pro Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met Tyr Met
575 580 585
Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro
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Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile
605 610 615
Val Ile Phe Phe Ser Val Leu Gly Val Val Phe Gly Lys Gly Asn
620 625 630
Thr Ala Phe Trp Ile Val Phe Ser Ile Ile His Ile Ile Ala Thr
635 640 645
Leu Leu Leu Ser Thr Gln Leu Tyr Tyr Met Gly Arg Trp Lys Leu
650 655 660
Asp Ser Gly Ile Phe Arg Arg Ile Leu His Val Leu Tyr Thr Asp
665 670 675
Cys Ile Arg Gln Cys Ser Gly Pro Leu Tyr Val Asp Arg Met Val
680 685 690
Leu Leu Val Met Gly Asn Val Ile Asn Trp Ser Leu Ala Ala Tyr

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Gly Leu Ile Met Arg Pro Asn Asp Phe Ala Ser Tyr Leu Leu Ala		
710	715	720
Ile Gly Ile Cys Asn Leu Leu Leu Tyr Phe Ala Phe Tyr Ile Ile		
725	730	735
Met Lys Leu Arg Ser Gly Glu Arg Ile Lys Leu Ile Pro Leu Leu		
740	745	750
Cys Ile Val Cys Thr Ser Val Val Trp Gly Phe Ala Leu Phe Phe		
755	760	765
Phe Phe Gln Gly Leu Ser Thr Trp Gln Lys Thr Pro Ala Glu Ser		
770	775	780
Arg Glu His Asn Arg Asp Cys Ile Leu Leu Asp Phe Phe Asp Asp		
785	790	795
His Asp Ile Trp His Phe Leu Ser Ser Ile Ala Met Phe Gly Ser		
800	805	810
Phe Leu Val Leu Leu Thr Leu Asp Asp Asp Leu Asp Thr Val Gln		
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Arg Asp Lys Ile Tyr Val Phe		
830		

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 <213> Homo sapiens

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<211> 807
<212> PRT
<213> Homo sapiens

<400> 229
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35 40 45
Leu Pro Arg Glu Gly Ala Glu Gly Gln Ile Val Leu Ser Gly Asp
50 55 60
Ser Gly Lys Ala Thr Glu Gly Pro Phe Ala Met Asp Pro Asp Ser
65 70 75
Gly Phe Leu Leu Val Thr Arg Ala Leu Asp Arg Glu Glu Gln Ala

80 85 90
Glu Tyr Gln Leu Gln Val Thr Leu Glu Met Gln Asp Gly His Val
95 100 105
Leu Trp Gly Pro Gln Pro Val Leu Val His Val Lys Asp Glu Asn
110 115 120
Asp Gln Val Pro His Phe Ser Gln Ala Ile Tyr Arg Ala Arg Leu
125 130 135
Ser Arg Gly Thr Arg Pro Gly Ile Pro Phe Leu Phe Leu Glu Ala
140 145 150
Ser Asp Arg Asp Glu Pro Gly Thr Ala Asn Ser Asp Leu Arg Phe
155 160 165
His Ile Leu Ser Gln Ala Pro Ala Gln Pro Ser Pro Asp Met Phe
170 175 180
Gln Leu Glu Pro Arg Leu Gly Ala Leu Ala Leu Ser Pro Lys Gly
185 190 195
Ser Thr Ser Leu Asp His Ala Leu Glu Arg Thr Tyr Gln Leu Leu
200 205 210
Val Gln Val Lys Asp Met Gly Asp Gln Ala Ser Gly His Gln Ala
215 220 225
Thr Ala Thr Val Glu Val Ser Ile Ile Glu Ser Thr Trp Val Ser
230 235 240
Leu Glu Pro Ile His Leu Ala Glu Asn Leu Lys Val Leu Tyr Pro
245 250 255
His His Met Ala Gln Val His Trp Ser Gly Gly Asp Val His Tyr
260 265 270
His Leu Glu Ser His Pro Pro Gly Pro Phe Glu Val Asn Ala Glu
275 280 285
Gly Asn Leu Tyr Val Thr Arg Glu Leu Asp Arg Glu Ala Gln Ala
290 295 300
Glu Tyr Leu Leu Gln Val Arg Ala Gln Asn Ser His Gly Glu Asp
305 310 315
Tyr Ala Ala Pro Leu Glu Leu His Val Leu Val Met Asp Glu Asn
320 325 330
Asp Asn Val Pro Ile Cys Pro Pro Arg Asp Pro Thr Val Ser Ile
335 340 345
Pro Glu Leu Ser Pro Pro Gly Thr Glu Val Thr Arg Leu Ser Ala
350 355 360
Glu Asp Ala Asp Ala Pro Gly Ser Pro Asn Ser His Val Val Tyr

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Gln Leu Leu Ser Pro Glu Pro Glu Asp Gly Val Glu Gly Arg Ala			
380	385	390	
Phe Gln Val Asp Pro Thr Ser Gly Ser Val Thr Leu Gly Val Leu			
395	400	405	
Pro Leu Arg Ala Gly Gln Asn Ile Leu Leu Leu Val Leu Ala Met			
410	415	420	
Asp Leu Ala Gly Ala Glu Gly Gly Phe Ser Ser Thr Cys Glu Val			
425	430	435	
Glu Val Ala Val Thr Asp Ile Asn Asp His Ala Pro Glu Phe Ile			
440	445	450	
Thr Ser Gln Ile Gly Pro Ile Ser Leu Pro Glu Asp Val Glu Pro			
455	460	465	
Gly Thr Leu Val Ala Met Leu Thr Ala Ile Asp Ala Asp Leu Glu			
470	475	480	
Pro Ala Phe Arg Leu Met Asp Phe Ala Ile Glu Arg Gly Asp Thr			
485	490	495	
Glu Gly Thr Phe Gly Leu Asp Trp Glu Pro Asp Ser Gly His Val			
500	505	510	
Arg Leu Arg Leu Cys Lys Asn Leu Ser Tyr Glu Ala Ala Pro Ser			
515	520	525	
His Glu Val Val Val Val Val Gln Ser Val Ala Lys Leu Val Gly			
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Pro Gly Pro Gly Pro Gly Ala Thr Ala Thr Val Thr Val Leu Val			
545	550	555	
Glu Arg Val Met Pro Pro Pro Lys Leu Asp Gln Glu Ser Tyr Glu			
560	565	570	
Ala Ser Val Pro Ile Ser Ala Pro Ala Gly Ser Phe Leu Leu Thr			
575	580	585	
Ile Gln Pro Ser Asp Pro Ile Ser Arg Thr Leu Arg Phe Ser Leu			
590	595	600	
Val Asn Asp Ser Glu Gly Trp Leu Cys Ile Glu Lys Phe Ser Gly			
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Glu Val His Thr Ala Gln Ser Leu Gln Gly Ala Gln Pro Gly Asp			
620	625	630	
Thr Tyr Thr Val Leu Val Glu Ala Gln Asp Thr Ala Leu Thr Leu			
635	640	645	
Ala Pro Val Pro Ser Gln Tyr Leu Cys Thr Pro Arg Gln Asp His			

650 655 660
Gly Leu Ile Val Ser Gly Pro Ser Lys Asp Pro Asp Leu Ala Ser
665 670 675
Gly His Gly Pro Tyr Ser Phe Thr Leu Gly Pro Asn Pro Thr Val
680 685 690
Gln Arg Asp Trp Arg Leu Gln Thr Leu Asn Gly Ser His Ala Tyr
695 700 705
Leu Thr Leu Ala Leu His Trp Val Glu Pro Arg Glu His Ile Ile
710 715 720
Pro Val Val Val Ser His Asn Ala Gln Met Trp Gln Leu Leu Val
725 730 735
Arg Val Ile Val Cys Arg Cys Asn Val Glu Gly Gln Cys Met Arg
740 745 750
Lys Val Gly Arg Met Lys Gly Met Pro Thr Lys Leu Ser Ala Val
755 760 765
Gly Ile Leu Val Gly Thr Leu Val Ala Ile Gly Ile Phe Leu Ile
770 775 780
Leu Ile Phe Thr His Trp Thr Met Ser Arg Lys Lys Asp Pro Asp
785 790 795
Gln Pro Ala Asp Ser Val Pro Leu Lys Ala Thr Val
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<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 230

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<210> 231

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 231

cctgagctgt aaccccactc cagg 24

<210> 232

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 232

agagtctgtc ccagctatct tgt 23

<210> 233

<211> 2786

<212> DNA

<213> Homo sapiens

<400> 233

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cagaaatgga gacgagatca gcaaatttag tcaactagtg aattcaaaca 150

acttgaagct caatttctgg aaatctccct cctccttcaa tcggcctgtg 200

gatgtcctgg tcccacatctgt cagtctgcag gcatttaaat ctttccttag 250

atcccagggc ttagagtacg cagtgacaat tgaggacctg caggcccttt 300

tagacaatga agatgatgaa atgcaacaca atgaagggc agaacggagc 350

agtaataact tcaactacgg ggcttaccat tccctggaag ctatttacca 400

cgagatggac aacattgccg cagactttcc tgacctggcg aggagggtga 450

agattggaca ttcgttgaa aaccggccga tgtatgtact gaagttcagc 500

actggaaag gcgtgaggcg gccggccgtt tggctgaatg caggcatcca 550

ttcccgagag tggatctccc aggccactgc aatctggacg gcaaggaaga 600

ttgtatctga ttaccagagg gatccagcta tcacccat cttggagaaa 650

atggatattt tcttgtgcc tgtggccaat cctgatggat atgtgtatac 700

tcaaactcaa aaccgattat ggaggaagac gcggccccga aatcctggaa 750

gctcctgcat tggtgctgac ccaaataagaa actggaacgc tagtttgca 800

ggaaaggag ccagcgacaa cccttgctcc gaagtgtacc atggacccca 850

cgc当地 attcg gaagtggagg taaaatcagt ggtagatttc atccaaaaac 900

atgggaattt caaggcttc atcgacactgc acagctactc gcagctgctg 950

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<210> 234
<211> 421
<212> PRT
<213> Homo sapiens

<400> 234
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Cys Gly Gln Glu Lys Phe Phe Gly Asp Gln Val Leu Arg Ile Asn
20 25 30
Val Arg Asn Gly Asp Glu Ile Ser Lys Leu Ser Gln Leu Val Asn
35 40 45
Ser Asn Asn Leu Lys Leu Asn Phe Trp Lys Ser Pro Ser Ser Phe
50 55 60
Asn Arg Pro Val Asp Val Leu Val Pro Ser Val Ser Leu Gln Ala
65 70 75
Phe Lys Ser Phe Leu Arg Ser Gln Gly Leu Glu Tyr Ala Val Thr
80 85 90
Ile Glu Asp Leu Gln Ala Leu Leu Asp Asn Glu Asp Asp Glu Met
95 100 105
Gln His Asn Glu Gly Gln Glu Arg Ser Ser Asn Asn Phe Asn Tyr
110 115 120
Gly Ala Tyr His Ser Leu Glu Ala Ile Tyr His Glu Met Asp Asn
125 130 135
Ile Ala Ala Asp Phe Pro Asp Leu Ala Arg Arg Val Lys Ile Gly
140 145 150
His Ser Phe Glu Asn Arg Pro Met Tyr Val Leu Lys Phe Ser Thr
155 160 165
Gly Lys Gly Val Arg Arg Pro Ala Val Trp Leu Asn Ala Gly Ile
170 175 180
His Ser Arg Glu Trp Ile Ser Gln Ala Thr Ala Ile Trp Thr Ala
185 190 195

Arg Lys Ile Val Ser Asp Tyr Gln Arg Asp Pro Ala Ile Thr Ser
200 205 210

Ile Leu Glu Lys Met Asp Ile Phe Leu Leu Pro Val Ala Asn Pro
215 220 225

Asp Gly Tyr Val Tyr Thr Gln Thr Gln Asn Arg Leu Trp Arg Lys
230 235 240

Thr Arg Ser Arg Asn Pro Gly Ser Ser Cys Ile Gly Ala Asp Pro
245 250 255

Asn Arg Asn Trp Asn Ala Ser Phe Ala Gly Lys Gly Ala Ser Asp
260 265 270

Asn Pro Cys Ser Glu Val Tyr His Gly Pro His Ala Asn Ser Glu
275 280 285

Val Glu Val Lys Ser Val Val Asp Phe Ile Gln Lys His Gly Asn
290 295 300

Phe Lys Gly Phe Ile Asp Leu His Ser Tyr Ser Gln Leu Leu Met
305 310 315

Tyr Pro Tyr Gly Tyr Ser Val Lys Lys Ala Pro Asp Ala Glu Glu
320 325 330

Leu Asp Lys Val Ala Arg Leu Ala Ala Lys Ala Leu Ala Ser Val
335 340 345

Ser Gly Thr Glu Tyr Gln Val Gly Pro Thr Cys Thr Thr Val Tyr
350 355 360

Pro Ala Ser Gly Ser Ser Ile Asp Trp Ala Tyr Asp Asn Gly Ile
365 370 375

Lys Phe Ala Phe Thr Phe Glu Leu Arg Asp Thr Gly Thr Tyr Gly
380 385 390

Phe Leu Leu Pro Ala Asn Gln Ile Ile Pro Thr Ala Glu Glu Thr
395 400 405

Trp Leu Gly Leu Lys Thr Ile Met Glu His Val Arg Asp Asn Leu
410 415 420

Tyr

<210> 235
<211> 1743
<212> DNA
<213> Homo sapiens

<400> 235
caaccatgca aggacagggc aggagaagag gaacctgcaa agacatattt 50

tgttccaaaa tggcatctta cctttatgga gtactcttg ctgttggcct 100

ctgtgctcca atctactgtg tgtccccggc caatgcccc agtgcataacc 150
cccgcccttc ctccacaaaag agcacccctg cctcacaggt gtattccctc 200
aacaccgact ttgccttccg cctataccgc aggctggttt tggagacccc 250
gagtcagaac atcttcttct cccctgttag tgcactccact tccctggcca 300
tgctctccct tggggcccac tcagtcacca agacccagat tctccaggc 350
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ttcttggca atgtcaagag gctgtatgaa gcagaagtct tttctacaga 550
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1743

<210> 236

<211> 417

<212> PRT

<213> Homo sapiens

<400> 236

Met Ala Ser Tyr Leu Tyr Gly Val Leu Phe Ala Val Gly Leu Cys
1 5 10 15

Ala Pro Ile Tyr Cys Val Ser Pro Ala Asn Ala Pro Ser Ala Tyr
20 25 30

Pro Arg Pro Ser Ser Thr Lys Ser Thr Pro Ala Ser Gln Val Tyr
35 40 45

Ser Leu Asn Thr Asp Phe Ala Phe Arg Leu Tyr Arg Arg Leu Val
50 55 60

Leu Glu Thr Pro Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Val
65 70 75

Ser Thr Ser Leu Ala Met Leu Ser Leu Gly Ala His Ser Val Thr
80 85 90

Lys Thr Gln Ile Leu Gln Gly Leu Gly Phe Asn Leu Thr His Thr
95 100 105

Pro Glu Ser Ala Ile His Gln Gly Phe Gln His Leu Val His Ser
110 115 120

Leu Thr Val Pro Ser Lys Asp Leu Thr Leu Lys Met Gly Ser Ala
125 130 135

Leu Phe Val Lys Lys Glu Leu Gln Leu Gln Ala Asn Phe Leu Gly
140 145 150

Asn Val Lys Arg Leu Tyr Glu Ala Glu Val Phe Ser Thr Asp Phe
155 160 165

Ser Asn Pro Ser Ile Ala Gln Ala Arg Ile Asn Ser His Val Lys
170 175 180

Lys Lys Thr Gln Gly Lys Val Val Asp Ile Ile Gln Gly Leu Asp
185 190 195

Leu Leu Thr Ala Met Val Leu Val Asn His Ile Phe Phe Lys Ala
200 205 210

Lys Trp Glu Lys Pro Phe His Leu Glu Tyr Thr Arg Lys Asn Phe
215 220 225

Pro Phe Leu Val Gly Glu Gln Val Thr Val Gln Val Pro Met Met
230 235 240

His Gln Lys Glu Gln Phe Ala Phe Gly Val Asp Thr Glu Leu Asn
245 250 255

Cys Phe Val Leu Gln Met Asp Tyr Lys Gly Asp Ala Val Ala Phe
260 265 270

Phe Val Leu Pro Ser Lys Gly Lys Met Arg Gln Leu Glu Gln Ala
275 280 285

Leu Ser Ala Arg Thr Leu Ile Lys Trp Ser His Ser Leu Gln Lys
290 295 300

Arg Trp Ile Glu Val Phe Ile Pro Arg Phe Ser Ile Ser Ala Ser
305 310 315

Tyr Asn Leu Glu Thr Ile Leu Pro Lys Met Gly Ile Gln Asn Ala
320 325 330

Phe Asp Lys Asn Ala Asp Phe Ser Gly Ile Ala Lys Arg Asp Ser
335 340 345

Leu Gln Val Ser Lys Ala Thr His Lys Ala Val Leu Asp Val Ser
350 355 360

Glu Glu Gly Thr Glu Ala Thr Ala Ala Thr Thr Thr Lys Phe Ile
365 370 375

Val Arg Ser Lys Asp Gly Pro Ser Tyr Phe Thr Val Ser Phe Asn
380 385 390

Arg Thr Phe Leu Met Met Ile Thr Asn Lys Ala Thr Asp Gly Ile
395 400 405

Leu Phe Leu Gly Lys Val Glu Asn Pro Thr Lys Ser
410 415

<210> 237

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 237

caaccatgca aggacagggc agg 23

<210> 238

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 238
cttgctgtt ggcctctgtg ctcccaacca tgcaaggaca gggcagg 47

<210> 239

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 239
tgactcgggg tctccaaaac cagc 24

<210> 240

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 240
ggtataggcg gaaggcaaag tcgg 24

<210> 241

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 241
ggcatttac cttaggag tactcttgc tgtggcctc tgtgctcc 48

<210> 242

<211> 2436

<212> DNA

<213> Homo sapiens

<400> 242
ggctgaccgt gctacattgc ctggaggaag cctaaggaac ccaggcatcc 50

agctgcccac gcctgagtcc aagattcttc ccaggaacac aaacgttagga 100

gacccacgct cctggaagca ccagccttta tctcttcacc ttcaagtccc 150

ctttctcaag aatcctctgt tctttgcctt ctaaagtctt ggtacatcta 200

ggacccaggc atcttgctt ccagccacaa agagacagat gaagatgcag 250

aaaggaaatg ttctccttat gtttggtcta ctattgcatt tagaagctgc 300
aacaaaattcc aatgagacta gcacacctgc caacactgga tccagtgtga 350
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tcaaaaatctc cacagtaaaa tccaaagacc taaaaaaaaaaaaaaa 2400
aaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaa 2436

<210> 243
<211> 596
<212> PRT
<213> Homo sapiens

<400> 243
Met Lys Met Gln Lys Gly Asn Val Leu Leu Met Phe Gly Leu Leu
1 5 10 15
Leu His Leu Glu Ala Ala Thr Asn Ser Asn Glu Thr Ser Thr Ser
20 25 30
Ala Asn Thr Gly Ser Ser Val Ile Ser Ser Gly Ala Ser Thr Ala
35 40 45
Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Val Ser Thr Ala
50 55 60
Thr Ile Ser Gly Ser Ser Val Thr Ser Asn Gly Val Ser Ile Val
65 70 75
Thr Asn Ser Glu Phe His Thr Thr Ser Ser Gly Ile Ser Thr Ala
80 85 90
Thr Asn Ser Glu Phe Ser Thr Ala Ser Ser Gly Ile Ser Ile Ala
95 100 105

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
110 115 120

Thr Asn Ser Glu Ser Ser Thr Pro Ser Ser Gly Ala Ser Thr Val
125 130 135

Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Ala Ser Thr Ala
140 145 150

Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Arg Ala Ser Thr Ala
155 160 165

Thr Asn Ser Glu Ser Ser Thr Leu Ser Ser Gly Ala Ser Thr Ala
170 175 180

Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
185 190 195

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
200 205 210

Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Arg Ala Ser Thr Ala
215 220 225

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
230 235 240

Thr Asn Ser Glu Ser Arg Thr Thr Ser Asn Gly Ala Gly Thr Ala
245 250 255

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
260 265 270

Thr Asn Ser Asp Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala
275 280 285

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
290 295 300

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
305 310 315

Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Gly Thr Ala
320 325 330

Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val
335 340 345

Thr Asn Ser Glu Ser Ser Thr Pro Ser Ser Gly Ala Asn Thr Ala
350 355 360

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala
365 370 375

Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala
380 385 390

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Val Ser Thr Ala
395 400 405

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
410 415 420

Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
425 430 435

Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val
440 445 450

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala
455 460 465

Thr Asn Ser Gly Ser Ser Val Thr Ser Ala Gly Ser Gly Thr Ala
470 475 480

Ala Leu Thr Gly Met His Thr Thr Ser His Ser Ala Ser Thr Ala
485 490 495

Val Ser Glu Ala Lys Pro Gly Gly Ser Leu Val Pro Trp Glu Ile
500 505 510

Phe Leu Ile Thr Leu Val Ser Val Val Ala Ala Val Gly Leu Phe
515 520 525

Ala Gly Leu Phe Phe Cys Val Arg Asn Ser Leu Ser Leu Arg Asn
530 535 540

Thr Phe Asn Thr Ala Val Tyr His Pro His Gly Leu Asn His Gly
545 550 555

Leu Gly Pro Gly Pro Gly Gly Asn His Gly Ala Pro His Arg Pro
560 565 570

Arg Trp Ser Pro Asn Trp Phe Trp Arg Arg Pro Val Ser Ser Ile
575 580 585

Ala Met Glu Met Ser Gly Arg Asn Ser Gly Pro
590 595

<210> 244

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 244

gaagcaccag cctttatctc ttcacc 26

<210> 245

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 245
gtcagagttg gtggctgtgc tagc 24

<210> 246
<211> 48
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 246
ggaccaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247
<211> 957
<212> DNA
<213> Homo sapiens

<400> 247
gggagagagg ataaatagca gctggcttc cttggctcct ctctgcattcc 50
ttcccgacct tcccagcaat atgcatttg cacgtctggt cggctcctgc 100
tccctccttc tgctactggg gcccctgtct ggatggcgcc ccagcgatga 150
ccccatttag aaggtcattt aaggatcaa ccgagggtcg agcaatgcag 200
agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgtcat 250
gccggaaggg aagtggagaa gttttcaac ggacttagca acatggggag 300
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gaagcagaga agcttggcca tggggtcaac aacgctgctg gacaggccgg 450
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ctggaaaggta agcagagaaaa cttggccaag gggtaacca tgctgctgac 550
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ccagcaagga ggccaaaccag ctgctgaatg gcaaccatca aagcggatct 700
tccagccatc aaggaggggc cacaaccacg ccgttagcct ctggggcctc 750
agtcaacacg ctttcatca accttccgc cctgtggagg agcgtcgcca 800

acatcatgcc ctaaactggc atccggcctt gctgggagaa taatgtcgcc 850
gttgtcacat cagctgacat gacctggagg ggttgggggt gggggacagg 900
tttctgaaat ccctgaaggg gtttgactg ggatttgcataaaacttga 950
tacacca 957

<210> 248
<211> 247
<212> PRT
<213> Homo sapiens

<400> 248
Met His Leu Ala Arg Leu Val Gly Ser Cys Ser Leu Leu Leu
1 5 10 15
Leu Gly Ala Leu Ser Gly Trp Ala Ala Ser Asp Asp Pro Ile Glu
20 25 30
Lys Val Ile Glu Gly Ile Asn Arg Gly Leu Ser Asn Ala Glu Arg
35 40 45
Glu Val Gly Lys Ala Leu Asp Gly Ile Asn Ser Gly Ile Thr His
50 55 60
Ala Gly Arg Glu Val Glu Lys Val Phe Asn Gly Leu Ser Asn Met
65 70 75
Gly Ser His Thr Gly Lys Glu Leu Asp Lys Gly Val Gln Gly Leu
80 85 90
Asn His Gly Met Asp Lys Val Ala His Glu Ile Asn His Gly Ile
95 100 105
Gly Gln Ala Gly Lys Glu Ala Glu Lys Leu Gly His Gly Val Asn
110 115 120
Asn Ala Ala Gly Gln Ala Gly Lys Glu Ala Asp Lys Ala Val Gln
125 130 135
Gly Phe His Thr Gly Val His Gln Ala Gly Lys Glu Ala Glu Lys
140 145 150
Leu Gly Gln Gly Val Asn His Ala Ala Asp Gln Ala Gly Lys Glu
155 160 165
Val Glu Lys Leu Gly Gln Gly Ala His His Ala Ala Gly Gln Ala
170 175 180
Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn Gln Ala Ser
185 190 195
Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser Gly Ser
200 205 210
Ser Ser His Gln Gly Gly Ala Thr Thr Thr Pro Leu Ala Ser Gly

215 220 225
Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg
230 235 240
Ser Val Ala Asn Ile Met Pro
245

<210> 249
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 249
 caaataatgcattt cttgcacgtc tgg 23

<210> 250
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 250
 aagctttctctt gcttcctttc ctgc 24

<210> 251
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 251
 tgacccccattt gagaagggtca ttgaagggtt caaccgaggg ctg 43

<210> 252
<211> 3781
<212> DNA
<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

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				20					25				30	

Leu	Leu	Leu	Leu	Gln	Pro	Pro	Pro	Thr	Trp	Ala	Leu	Ser	
				35				40				45	

Pro	Arg	Ile	Ser	Leu	Pro	Leu	Gly	Ser	Glu	Glu	Arg	Pro	Phe	Leu
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Arg	Phe	Glu	Ala	Glu	His	Ile	Ser	Asn	Tyr	Thr	Ala	Leu	Leu	
					65				70				75	

Ser	Arg	Asp	Gly	Arg	Thr	Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Leu
					80				85				90	

Phe	Ala	Leu	Ser	Ser	Asn	Leu	Ser	Phe	Leu	Pro	Gly	Gly	Glu	Tyr
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Gln	Glu	Leu	Leu	Trp	Gly	Ala	Asp	Ala	Glu	Lys	Lys	Gln	Gln	Cys
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Ser Phe Lys Gly Lys Asp Pro Gln Arg Asp Cys Gln Asn Tyr Ile
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Lys Ile Leu Leu Pro Leu Ser Gly Ser His Leu Phe Thr Cys Gly
140 145 150

Thr Ala Ala Phe Ser Pro Met Cys Thr Tyr Ile Asn Met Glu Asn
155 160 165

Phe Thr Leu Ala Arg Asp Glu Lys Gly Asn Val Leu Leu Glu Asp
170 175 180

Gly Lys Gly Arg Cys Pro Phe Asp Pro Asn Phe Lys Ser Thr Ala
185 190 195

Leu Val Val Asp Gly Glu Leu Tyr Thr Gly Thr Val Ser Ser Phe
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Gln Gly Asn Asp Pro Ala Ile Ser Arg Ser Gln Ser Leu Arg Pro
215 220 225

Thr Lys Thr Glu Ser Ser Leu Asn Trp Leu Gln Asp Pro Ala Phe
230 235 240

Val Ala Ser Ala Tyr Ile Pro Glu Ser Leu Gly Ser Leu Gln Gly
245 250 255

Asp Asp Asp Lys Ile Tyr Phe Phe Ser Glu Thr Gly Gln Glu
260 265 270

Phe Glu Phe Phe Glu Asn Thr Ile Val Ser Arg Ile Ala Arg Ile
275 280 285

Cys Lys Gly Asp Glu Gly Glu Arg Val Leu Gln Gln Arg Trp
290 295 300

Thr Ser Phe Leu Lys Ala Gln Leu Leu Cys Ser Arg Pro Asp Asp
305 310 315

Gly Phe Pro Phe Asn Val Leu Gln Asp Val Phe Thr Leu Ser Pro
320 325 330

Ser Pro Gln Asp Trp Arg Asp Thr Leu Phe Tyr Gly Val Phe Thr
335 340 345

Ser Gln Trp His Arg Gly Thr Thr Glu Gly Ser Ala Val Cys Val
350 355 360

Phe Thr Met Lys Asp Val Gln Arg Val Phe Ser Gly Leu Tyr Lys
365 370 375

Glu Val Asn Arg Glu Thr Gln Gln Trp Tyr Thr Val Thr His Pro
380 385 390

Val Pro Thr Pro Arg Pro Gly Ala Cys Ile Thr Asn Ser Ala Arg
395 400 405

Glu Arg Lys Ile Asn Ser Ser Leu Gln Leu Pro Asp Arg Val Leu
410 415 420

Asn Phe Leu Lys Asp His Phe Leu Met Asp Gly Gln Val Arg Ser
425 430 435

Arg Met Leu Leu Leu Gln Pro Gln Ala Arg Tyr Gln Arg Val Ala
440 445 450

Val His Arg Val Pro Gly Leu His His Thr Tyr Asp Val Leu Phe
455 460 465

Leu Gly Thr Gly Asp Gly Arg Leu His Lys Ala Val Ser Val Gly
470 475 480

Pro Arg Val His Ile Ile Glu Glu Leu Gln Ile Phe Ser Ser Gly
485 490 495

Gln Pro Val Gln Asn Leu Leu Leu Asp Thr His Arg Gly Leu Leu
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Tyr Ala Ala Ser His Ser Gly Val Val Gln Val Pro Met Ala Asn
515 520 525

Cys Ser Leu Tyr Arg Ser Cys Gly Asp Cys Leu Leu Ala Arg Asp
530 535 540

Pro Tyr Cys Ala Trp Ser Gly Ser Ser Cys Lys His Val Ser Leu
545 550 555

Tyr Gln Pro Gln Leu Ala Thr Arg Pro Trp Ile Gln Asp Ile Glu
560 565 570

Gly Ala Ser Ala Lys Asp Leu Cys Ser Ala Ser Ser Val Val Ser
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Pro Ser Phe Val Pro Thr Gly Glu Lys Pro Cys Glu Gln Val Gln
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Phe Gln Pro Asn Thr Val Asn Thr Leu Ala Cys Pro Leu Leu Ser
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Asn Leu Ala Thr Arg Leu Trp Leu Arg Asn Gly Ala Pro Val Asn
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Ala Ser Ala Ser Cys His Val Leu Pro Thr Gly Asp Leu Leu Leu
635 640 645

Val Gly Thr Gln Gln Leu Gly Glu Phe Gln Cys Trp Ser Leu Glu
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Glu Gly Phe Gln Gln Leu Val Ala Ser Tyr Cys Pro Glu Val Val
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Glu Asp Gly Val Ala Asp Gln Thr Asp Glu Gly Gly Ser Val Pro
680 685 690

Val Ile Ile Ser Thr Ser Arg Val Ser Ala Pro Ala Gly Gly Lys
695 700 705

Ala Ser Trp Gly Ala Asp Arg Ser Tyr Trp Lys Glu Phe Leu Val
710 715 720

Met Cys Thr Leu Phe Val Leu Ala Val Leu Leu Pro Val Leu Phe
725 730 735

Leu Leu Tyr Arg His Arg Asn Ser Met Lys Val Phe Leu Lys Gln
740 745 750

Gly Glu Cys Ala Ser Val His Pro Lys Thr Cys Pro Val Val Leu
755 760 765

Pro Pro Glu Thr Arg Pro Leu Asn Gly Leu Gly Pro Pro Ser Thr
770 775 780

Pro Leu Asp His Arg Gly Tyr Gln Ser Leu Ser Asp Ser Pro Pro
785 790 795

Gly Ala Arg Val Phe Thr Glu Ser Glu Lys Arg Pro Leu Ser Ile
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Gln Asp Ser Phe Val Glu Val Ser Pro Val Cys Pro Arg Pro Arg
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Val Arg Leu Gly Ser Glu Ile Arg Asp Ser Val Val
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<211> 802

<212> PRT

<213> Homo sapiens

<400> 260

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Glu Gly Cys Arg Ser Gly Gln Ala Ala Ala Ser Gln Ala Gly Gly
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Ala Arg Gly Asp Ala Arg Gly Ala Gln Leu Trp Pro Pro Gly Ser
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Asp Pro Asp Gly Gly Pro Arg Asp Arg Asn Phe Leu Phe Val Gly
80 85 90

Val Met Thr Ala Gln Lys Tyr Leu Gln Thr Arg Ala Val Ala Ala
95 100 105

Tyr Arg Thr Trp Ser Lys Thr Ile Pro Gly Lys Val Gln Phe Phe
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Ser Ser Glu Gly Ser Asp Thr Ser Val Pro Ile Pro Val Val Pro
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Leu Arg Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys Ser Phe
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Trp Phe Met Arg Ala Asp Asp Val Tyr Ile Lys Gly Asp Arg
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Leu Gly Gln Thr Gly Leu Gly Thr Thr Glu Glu Met Gly Lys Leu
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Ala Leu Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly Val
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Ile Met Ser Arg Glu Val Leu Arg Arg Met Val Pro His Ile Gly
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Lys Cys Leu Arg Glu Met Tyr Thr His Glu Asp Val Glu Val
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Gly Arg Cys Val Arg Arg Phe Ala Gly Val Gln Cys Val Trp Ser
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Tyr Glu Met Arg Gln Leu Phe Tyr Glu Asn Tyr Glu Gln Asn Lys

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Lys Gly Tyr Ile Arg Asp Leu His Asn Ser Lys Ile His Gln Ala
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His Ser Tyr Met Leu Ser Arg Lys Ile Ser Glu Leu Arg His Arg
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Thr Ile Gln Leu His Arg Glu Ile Val Leu Met Ser Lys Tyr Ser
335 340 345
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Pro Val Arg Arg His Ala Tyr Leu Gln Gln Thr Phe Ser Lys Ile
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Gln Phe Val Glu His Glu Glu Leu Asp Ala Gln Glu Leu Ala Lys
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Leu Lys Lys Leu Val Pro Phe Gln Leu Pro Gly Ser Lys Ser Glu
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Ser Gly Arg Phe Asp Met Phe Val Arg Phe Met Gly Asn Phe Glu
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Lys Thr Cys Leu Ile Pro Asn Gln Asn Val Lys Leu Val Val Leu

	560	565	570
Leu Phe Asn Ser Asp Ser Asn Pro Asp Lys Ala Lys Gln Val Glu	575	580	585
Leu Met Arg Asp Tyr Arg Ile Lys Tyr Pro Lys Ala Asp Met Gln	590	595	600
Ile Leu Pro Val Ser Gly Glu Phe Ser Arg Ala Leu Ala Leu Glu	605	610	615
Val Gly Ser Ser Gln Phe Asn Asn Glu Ser Leu Leu Phe Phe Cys	620	625	630
Asp Val Asp Leu Val Phe Thr Thr Glu Phe Leu Gln Arg Cys Arg	635	640	645
Ala Asn Thr Val Leu Gly Gln Gln Ile Tyr Phe Pro Ile Ile Phe	650	655	660
Ser Gln Tyr Asp Pro Lys Ile Val Tyr Ser Gly Lys Val Pro Ser	665	670	675
Asp Asn His Phe Ala Phe Thr Gln Lys Thr Gly Phe Trp Arg Asn	680	685	690
Tyr Gly Phe Gly Ile Thr Cys Ile Tyr Lys Gly Asp Leu Val Arg	695	700	705
Val Gly Gly Phe Asp Val Ser Ile Gln Gly Trp Gly Leu Glu Asp	710	715	720
Val Asp Leu Phe Asn Lys Val Val Gln Ala Gly Leu Lys Thr Phe	725	730	735
Arg Ser Gln Glu Val Gly Val Val His Val His His Pro Val Phe	740	745	750
Cys Asp Pro Asn Leu Asp Pro Lys Gln Tyr Lys Met Cys Leu Gly	755	760	765
Ser Lys Ala Ser Thr Tyr Gly Ser Thr Gln Gln Leu Ala Glu Met	770	775	780
Trp Leu Glu Lys Asn Asp Pro Ser Tyr Ser Lys Ser Ser Asn Asn	785	790	795
Asn Gly Ser Val Arg Thr Ala	800		

<210> 261

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 261
gtgccactac ggggtgtgga cgac 24

<210> 262
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 262
tcccatttct tccgtggtgc ccag 24

<210> 263
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 263
ccagaagaag tccttcatga tgctcaagta catgcacgac cactac 46

<210> 264
<211> 1419
<212> DNA
<213> Homo sapiens

<400> 264
ggacaaccgt tgctgggtgt cccaggcct gaggcaggac ggtactccgc 50
tgacacccctc ccttcggcc ttgaggttcc cagcctggtg gccccaggac 100
gttccggtcg catggcagag tgctacggac gacgcctatg aagcccttag 150
tccttctagt tgcgcttttgc ctatggcctt cgtctgtgcc ggcttatccg 200
agcataactg tgacacctga tgaagagcaa aacttgaatc attatataca 250
agtttttagag aaccttagtac gaagtgttcc ctctggggag ccaggtcgtg 300
agaaaaaaatc taactctcca aaacatgttt attctatagc atcaaaggga 350
tcaaaattta aggagctagt tacacatgga gacgcttcaa ctgagaatga 400
tgttttaacc aatcctatca gtgaagaaaac tacaactttc cctacaggag 450
gcttcacacc ggaaatagga aagaaaaaaac acacggaaag tacccttattc 500
tggtcgatca aaccaaacaa tgtttccatt gtttgcatg cagaggaacc 550
ttatattgaa aatgaagagc cagagccaga gccggagcca gctgcaaaac 600
aaactgaggc accaagaatg ttgccagttg ttactgaatc atctacaagt 650

ccatatgtta cctcatacaa gtcacctgtc accacttagt ataagagcac 700
tggcatttag atctctacag aatcagaaga tgttcctcag ctctcaggtg 750
aaactgcgt agaaaaaccc gaagagttt gaaagcaccc agagagttgg 800
aataatgtg acatttgaa aaaaattttt gatattaatt cacaagtgc 850
acaggcactt cttagtgaca ccagcaaccc agcatataga gaagatattt 900
aagcctctaa agatcaccta aaacgaagcc ttgctctagc agcagcagca 950
gaacataaat taaaaacaat gtataagtcc cagttattgc cagtaggacg 1000
aacaagtaat aaaattgtg acatcgaaac tgttattaac atgctgtgt 1050
attctagatc taaactctat gaatatttag atattaaatg tgttccacca 1100
gagatgagag aaaaagctgc tacagtattc aatacattaa aaaatatgtg 1150
tagatcaagg agagtcacag ctttattaa agtttattaa acaataat 1200
aaaaattttt aacctacttg atattccata acaaagctga tttaagcaaa 1250
ctgcatttt tcacaggaga aataatcata ttgcataattt caaaagttgt 1300
ataaaaaat tttctattgt agttcaaattg tgccaacatc tttatgtgtc 1350
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atttggttc aggaaaaaa 1419

<210> 265

<211> 350

<212> PRT

<213> Homo sapiens

<400> 265

Met	Lys	Pro	Leu	Val	Leu	Leu	Val	Ala	Leu	Leu	Leu	Trp	Pro	Ser
1			5					10				15		

Ser	Val	Pro	Ala	Tyr	Pro	Ser	Ile	Thr	Val	Thr	Pro	Asp	Glu	Glu
				20				25				30		

Gln	Asn	Leu	Asn	His	Tyr	Ile	Gln	Val	Leu	Glu	Asn	Leu	Val	Arg
				35				40				45		

Ser	Val	Pro	Ser	Gly	Glu	Pro	Gly	Arg	Glu	Lys	Lys	Ser	Asn	Ser
				50				55				60		

Pro	Lys	His	Val	Tyr	Ser	Ile	Ala	Ser	Lys	Gly	Ser	Lys	Phe	Lys
				65				70				75		

Glu	Leu	Val	Thr	His	Gly	Asp	Ala	Ser	Thr	Glu	Asn	Asp	Val	Leu
				80				85				90		

Thr Asn Pro Ile Ser Glu Glu Thr Thr Phe Pro Thr Gly Gly
95 100 105

Phe Thr Pro Glu Ile Gly Lys Lys His Thr Glu Ser Thr Pro
110 115 120

Phe Trp Ser Ile Lys Pro Asn Asn Val Ser Ile Val Leu His Ala
125 130 135

Glu Glu Pro Tyr Ile Glu Asn Glu Glu Pro Glu Pro Glu Pro Glu
140 145 150

Pro Ala Ala Lys Gln Thr Glu Ala Pro Arg Met Leu Pro Val Val
155 160 165

Thr Glu Ser Ser Thr Ser Pro Tyr Val Thr Ser Tyr Lys Ser Pro
170 175 180

Val Thr Thr Leu Asp Lys Ser Thr Gly Ile Glu Ile Ser Thr Glu
185 190 195

Ser Glu Asp Val Pro Gln Leu Ser Gly Glu Thr Ala Ile Glu Lys
200 205 210

Pro Glu Glu Phe Gly Lys His Pro Glu Ser Trp Asn Asn Asp Asp
215 220 225

Ile Leu Lys Lys Ile Leu Asp Ile Asn Ser Gln Val Gln Gln Ala
230 235 240

Leu Leu Ser Asp Thr Ser Asn Pro Ala Tyr Arg Glu Asp Ile Glu
245 250 255

Ala Ser Lys Asp His Leu Lys Arg Ser Leu Ala Leu Ala Ala Ala
260 265 270

Ala Glu His Lys Leu Lys Thr Met Tyr Lys Ser Gln Leu Leu Pro
275 280 285

Val Gly Arg Thr Ser Asn Lys Ile Asp Asp Ile Glu Thr Val Ile
290 295 300

Asn Met Leu Cys Asn Ser Arg Ser Lys Leu Tyr Glu Tyr Leu Asp
305 310 315

Ile Lys Cys Val Pro Pro Glu Met Arg Glu Lys Ala Ala Thr Val
320 325 330

Phe Asn Thr Leu Lys Asn Met Cys Arg Ser Arg Arg Val Thr Ala
335 340 345

Leu Leu Lys Val Tyr
350

<210> 266

<211> 2403

<212> DNA

<213> Homo sapiens

<400> 266

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acagctggcc tgacctccaa atcatccatc caccctgct gtcatctgtt 100
ttcatagtgt gagatcaacc cacaggaata tccatggctt ttgtgctcat 150
tttggttctc agtttctacg agctggtgctc aggacagtgg caagtactg 200
gaccggcaa gtttgtccag gccttggtg 999 gggaggacgc cgtgttctcc 250
tgctccctct ttcctgagac cagtgcagag gctatggaag tgcggttctt 300
caggaatcag ttccatgctg tggccaccc ctacagagat gggaaagact 350
ggaaatctaa gcagatgcc a cgtatcgag ggagaactga gtttgtgaag 400
gactccattg cagggggcg tgtctctcta aggctaaaaa acatcactcc 450
ctcggacatc ggcctgtatg ggtgctgggt cagttccag atttacgatg 500
aggaggccac ctgggagctg cgggtggcag cactgggctc acttcctctc 550
atttccatcg tggatatgt tgacggaggt atccagttac tctgcctgctc 600
ctcaggctgg ttcccccagc ccacagccaa gtggaaaggt ccacaaggac 650
aggatttgc ttcagactcc agagcaaatg cagatggta cagcctgtat 700
gatgtggaga tctccattat agtccaggaa aatgctggga gcatatttg 750
ttccatccac cttgctgagc agagtcatga ggtggaaatcc aaggtattga 800
taggagagac gttttccag ccctcacctt ggcgcctggc ttctatttt 850
ctcgggttac tctgtggtgc cctgtgtggt gttgtcatgg ggatgataat 900
tgttttcttc aaatccaaag ggaaaatcca ggcggaaactg gactggagaa 950
gaaaggcacgg acaggcagaa ttgagagacg cccggaaaca cgcagtggag 1000
gtgactctgg atccagagac ggctcacccg aagctctgctg tttctgatct 1050
gaaaactgta acccatagaa aagctccccaa ggaggtgcct cactctgaga 1100
agagatttac aaggaagagt gtggtggctt ctcagggttt ccaaggcaggg 1150
agacattact gggaggtgga cgtgggacaa aatgttagggt ggtatgtgg 1200
agtgtgtcg gatgacgtag acagggggaa gaacaatgtg actttgtctc 1250
ccaacaatgg gtattgggtc ctcagactga caacagaaca tttgtatttc 1300
acattcaatc cccattttat cagcctccccccc cccagcacc ctcctacacg 1350

agtaggggtc ttccctggact atgagggtgg gaccatctcc ttcttcaata 1400
caaatgacca gtcccttatt tataccctgc tgacatgtca gtttgaaggc 1450
ttgttgagac cctatatcca gcatgcgatg tatgacgagg aaaaggggac 1500
tcccatattc atatgtccag tgtcctgggg atgagacaga gaagaccotg 1550
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ttaggttag tttgtaaaaa ctccatccag ctaagcgatc ttgaacaagt 1850
cacaacctcc caggctcctc atttgcttagt cacggacagt gattcctgcc 1900
tcacaggtga agattaaaga gacaacgaat gtgaatcatg cttgcaggtt 1950
tgagggcaca gtgttgcta atgatgtgtt tttatattat acatttccc 2000
accataaaact ctgttgctt attccacatt aatttacttt tctctataacc 2050
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ataaagagga ggtaggattt ttcaactgatt ctataagccc agcattaccc 2150
gataccaaaa ccaggcaaag aaaacagaag aagaggaagg aaaactacag 2200
gtccatatcc ctcattaaca cagacacaaa aattctaaat aaaattttaa 2250
caaattaaac taaacaatat atttaaagat gatataaac tactcagtgt 2300
ggtttgcaccc acaaatgcag agttggtttta atatttaat atcaaccagt 2350
gtaattcagc acattaataa agtaaaaaag aaaaccataa aaaaaaaaaa 2400
aaa 2403

<210> 267
<211> 466
<212> PRT
<213> Homo sapiens

<400> 267
Met Ala Phe Val Leu Ile Leu Val Leu Ser Phe Tyr Glu Leu Val
1 5 10 15
Ser Gly Gln Trp Gln Val Thr Gly Pro Gly Lys Phe Val Gln Ala
20 25 30
Leu Val Gly Glu Asp Ala Val Phe Ser Cys Ser Leu Phe Pro Glu

	35	40	45
Thr Ser Ala Glu Ala Met Glu Val Arg Phe Phe Arg Asn Gln Phe			
50	55		60
His Ala Val Val His Leu Tyr Arg Asp Gly Glu Asp Trp Glu Ser			
65	70		75
Lys Gln Met Pro Gln Tyr Arg Gly Arg Thr Glu Phe Val Lys Asp			
80	85		90
Ser Ile Ala Gly Gly Arg Val Ser Leu Arg Leu Lys Asn Ile Thr			
95	100		105
Pro Ser Asp Ile Gly Leu Tyr Gly Cys Trp Phe Ser Ser Gln Ile			
110	115		120
Tyr Asp Glu Glu Ala Thr Trp Glu Leu Arg Val Ala Ala Leu Gly			
125	130		135
Ser Leu Pro Leu Ile Ser Ile Val Gly Tyr Val Asp Gly Gly Ile			
140	145		150
Gln Leu Leu Cys Leu Ser Ser Gly Trp Phe Pro Gln Pro Thr Ala			
155	160		165
Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Ser Asp Ser Arg			
170	175		180
Ala Asn Ala Asp Gly Tyr Ser Leu Tyr Asp Val Glu Ile Ser Ile			
185	190		195
Ile Val Gln Glu Asn Ala Gly Ser Ile Leu Cys Ser Ile His Leu			
200	205		210
Ala Glu Gln Ser His Glu Val Glu Ser Lys Val Leu Ile Gly Glu			
215	220		225
Thr Phe Phe Gln Pro Ser Pro Trp Arg Leu Ala Ser Ile Leu Leu			
230	235		240
Gly Leu Leu Cys Gly Ala Leu Cys Gly Val Val Met Gly Met Ile			
245	250		255
Ile Val Phe Phe Lys Ser Lys Gly Lys Ile Gln Ala Glu Leu Asp			
260	265		270
Trp Arg Arg Lys His Gly Gln Ala Glu Leu Arg Asp Ala Arg Lys			
275	280		285
His Ala Val Glu Val Thr Leu Asp Pro Glu Thr Ala His Pro Lys			
290	295		300
Leu Cys Val Ser Asp Leu Lys Thr Val Thr His Arg Lys Ala Pro			
305	310		315
Gln Glu Val Pro His Ser Glu Lys Arg Phe Thr Arg Lys Ser Val			

	320	325	330
Val Ala Ser Gln Gly Phe Gln Ala Gly Arg His Tyr Trp Glu Val			
335	340	345	
Asp Val Gly Gln Asn Val Gly Trp Tyr Val Gly Val Cys Arg Asp			
350	355	360	
Asp Val Asp Arg Gly Lys Asn Asn Val Thr Leu Ser Pro Asn Asn			
365	370	375	
Gly Tyr Trp Val Leu Arg Leu Thr Thr Glu His Leu Tyr Phe Thr			
380	385	390	
Phe Asn Pro His Phe Ile Ser Leu Pro Pro Ser Thr Pro Pro Thr			
395	400	405	
Arg Val Gly Val Phe Leu Asp Tyr Glu Gly Gly Thr Ile Ser Phe			
410	415	420	
Phe Asn Thr Asn Asp Gln Ser Leu Ile Tyr Thr Leu Leu Thr Cys			
425	430	435	
Gln Phe Glu Gly Leu Leu Arg Pro Tyr Ile Gln His Ala Met Tyr			
440	445	450	
Asp Glu Glu Lys Gly Thr Pro Ile Phe Ile Cys Pro Val Ser Trp			
455	460	465	

Gly

<210> 268
<211> 2103
<212> DNA
<213> Homo sapiens

<400> 268
ccttcacagg actcttcatt gctgggtggc aatgatgtat cggccagatg 50
tggtgagggc tagaaaaaga gtttgtggg aaccctgggt tatcggcctc 100
gtcatcttca tatccctgat tgtcctggca gtgtgcattg gactcactgt 150
tcattatgtg agatataatc aaaagaagac ctacaattac tatagcacat 200
tgtcatttac aactgacaaa ctatatgctg agtttggcag agaggctct 250
aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc 300
attttataaa tctccattaa gggagaatt tgtcaagtct caggttatca 350
agttcagtca acagaagcat ggagtgtgg ctcatatgct gttgatttgt 400
agatttcact ctactgagga tcctgaaact gtagataaaa ttgttcaact 450
tgttttacat gaaaagctgc aagatgctgt aggaccccct aaagtagatc 500

ctcactcagt taaaattaaa aaaatcaaca agacagaaac agacagctat 550
ctaaaccatt gctgcggaac acgaagaagt aaaactctag gtcagagtct 600
caggatcggtt ggtggacag aagtagaaga gggtaatgg ccctggcagg 650
ctagcctgca gtggatggg agtcatcgct gtggagcaac cttaattaaat 700
gccacatggc ttgtgagtgc tgctcactgt tttacaacat ataagaaccc 750
tgccagatgg actgcttctt ttggagtaac aataaaacct tcgaaaatga 800
aacgggtct ccggagaata attgtccatg aaaaatacaa acacccatca 850
catgactatg atatttctt tgcagagctt tctagccctg ttccctacac 900
aatgcagta catagagttt gtctccctga tgcatttat gagtttcaac 950
caggtgatgt gatgttgtg acaggattt gggactgaa aatgatggt 1000
tacagtcaaa atcatcttcg acaagcacag gtgactctca tagacgctac 1050
aacttgcaat gaacctcaag cttacaatga cgccataact cctagaatgt 1100
tatgtgctgg ctccttagaa ggaaaaacag atgcattgcca gggtgactct 1150
ggaggaccac tggtagttc agatgctaga gatatctggt accttgctgg 1200
aatagtgagc tggggagatg aatgtgcgaa acccaacaag cctgggttt 1250
atactagagt tacggcctt cgggactgga ttacttcaaa aactggtac 1300
taagagacaa aagcctcatg gaacagataa cattttttt tgtttttgg 1350
gtgtggaggc catttttaga gatacagaat tggagaagac ttgcaaaaca 1400
gctagattt actgatctca ataaactgtt tgcttgatgc atgtatccc 1450
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cagaattttt acttggacataaattgtt aatgcattata tacaatttga 1650
agcaactcctt ttcttcagtt cctcagctcc tctcatttca gcaaatatcc 1700
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tcccctacat ttattggca cagaaaagta ttaggtgttt ttcttagtgg 1800
aatattagaa atgatcatat tcattatgaa aggtcaagca aagacagcag 1850
aataccaatc acttcatcat ttaggaagta tggaaactaa gttaaggaag 1900

tccagaaaaga agccaaagata tatccttatt ttcatttcca aacaactact 1950
atgataaaatg tgaagaagat tctgttttt tgtgacctat aataattata 2000
caaacttcat gcaatgtact tggtaaggc aaattaaagc aaatatttat 2050
ttaacattgt tactgaggat gtcaacatat aacaataaaa tataaatcac 2100
cca 2103

<210> 269
<211> 423
<212> PRT
<213> Homo sapiens

<400> 269
Met Met Tyr Arg Pro Asp Val Val Arg Ala Arg Lys Arg Val Cys
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Trp Glu Pro Trp Val Ile Gly Leu Val Ile Phe Ile Ser Leu Ile
20 25 30

Val Leu Ala Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr
35 40 45

Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr
50 55 60

Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn
65 70 75

Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala
80 85 90

Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val
95 100 105

Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu
110 115 120

Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp
125 130 135

Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val
140 145 150

Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile
155 160 165

Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr
170 175 180

Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly
185 190 195

Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln
200 205 210

Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr
 215 220 225
 Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro
 230 235 240
 Ala Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys
 245 250 255
 Met Lys Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys
 260 265 270
 His Pro Ser His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser
 275 280 285
 Pro Val Pro Tyr Thr Asn Ala Val His Arg Val Cys Leu Pro Asp
 290 295 300
 Ala Ser Tyr Glu Phe Gln Pro Gly Asp Val Met Phe Val Thr Gly
 305 310 315
 Phe Gly Ala Leu Lys Asn Asp Gly Tyr Ser Gln Asn His Leu Arg
 320 325 330
 Gln Ala Gln Val Thr Leu Ile Asp Ala Thr Thr Cys Asn Glu Pro
 335 340 345
 Gln Ala Tyr Asn Asp Ala Ile Thr Pro Arg Met Leu Cys Ala Gly
 350 355 360
 Ser Leu Glu Gly Lys Thr Asp Ala Cys Gln Gly Asp Ser Gly Gly
 365 370 375
 Pro Leu Val Ser Ser Asp Ala Arg Asp Ile Trp Tyr Leu Ala Gly
 380 385 390
 Ile Val Ser Trp Gly Asp Glu Cys Ala Lys Pro Asn Lys Pro Gly
 395 400 405
 Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile Thr Ser Lys
 410 415 420
 Thr Gly Ile

<210> 270
 <211> 1170
 <212> DNA
 <213> Homo sapiens

<400> 270
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 aacctgacag cacagcctga gatcttgggg atccctcagc ctaacaccca 100
 cagacgtcag ctggtgatt cccgctgcat caaggcctac ccactgtctc 150

catgctggc tctccctgcc ttctgtggct cctggccgtg accttcttgg 200
ttcccagagc tcagcccttg gcccctcaag actttgaaga agaggaggca 250
gatgagactg agacggcgtg gccgccttg ccggctgtcc cctgcgacta 300
cgaccactgc cgacacactgc aggtgccctg caaggagcta cagagggtcg 350
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gaccgcgc gcatgggaga agtgcgcatt gcggccgaag agggccgcgc 450
agtggtccac tggtgtgccc cttctccccc gtcctccac tactggctgc 500
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acggtccgca gagccgaact gaaggggctg aagccagggg gcatttatgt 600
cgtttgcgta gtggccgcta acgaggccgg ggcaagccgc gtgccccagg 650
ctggaggaga gggcctcgag ggggcccaca tccctgcctt cgggccttgc 700
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gccgcagggg cgctctgaaa ggggcctggg ggcatactcg gcacagacag 900
ccccacctgg ggcgcatacg ctggcccccgg ggaaagagga aaacccgctg 950
cctccaggaa gggctggacg gcgagctggg agccagccccc aggctccagg 1000
gccacggcgg agtcatggtt ctcaggactg agcgcttggtaggtccgg 1050
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ccccaaatttt ttttaagcg gccagataat aaataatgta acctttgcgg 1150
ttaaaaaaaaaaaaaaa 1170

<210> 271
<211> 238
<212> PRT
<213> Homo sapiens

<400> 271
Met Leu Gly Ser Pro Cys Leu Leu Trp Leu Leu Ala Val Thr Phe
1 5 10 15
Leu Val Pro Arg Ala Gln Pro Leu Ala Pro Gln Asp Phe Glu Glu
20 25 30
Glu Glu Ala Asp Glu Thr Glu Thr Ala Trp Pro Pro Leu Pro Ala
35 40 45

Val Pro Cys Asp Tyr Asp His Cys Arg His Leu Gln Val Pro Cys
50 55 60

Lys Glu Leu Gln Arg Val Gly Pro Ala Ala Cys Leu Cys Pro Gly
65 70 75

Leu Ser Ser Pro Ala Gln Pro Pro Asp Pro Pro Arg Met Gly Glu
80 85 90

Val Arg Ile Ala Ala Glu Glu Gly Arg Ala Val Val His Trp Cys
95 100 105

Ala Pro Phe Ser Pro Val Leu His Tyr Trp Leu Leu Leu Trp Asp
110 115 120

Gly Ser Glu Ala Ala Gln Lys Gly Pro Pro Leu Asn Ala Thr Val
125 130 135

Arg Arg Ala Glu Leu Lys Gly Leu Lys Pro Gly Gly Ile Tyr Val
140 145 150

Val Cys Val Val Ala Ala Asn Glu Ala Gly Ala Ser Arg Val Pro
155 160 165

Gln Ala Gly Gly Glu Gly Leu Glu Gly Ala Asp Ile Pro Ala Phe
170 175 180

Gly Pro Cys Ser Arg Leu Ala Val Pro Pro Asn Pro Arg Thr Leu
185 190 195

Val His Ala Ala Val Gly Val Gly Thr Ala Leu Ala Leu Leu Ser
200 205 210

Cys Ala Ala Leu Val Trp His Phe Cys Leu Arg Asp Arg Trp Gly
215 220 225

Cys Pro Arg Arg Ala Ala Ala Arg Ala Ala Gly Ala Leu
230 235

<210> 272
<211> 2397
<212> DNA
<213> Homo sapiens

<400> 272
agagaaaagaa gcgtctccag ctgaagccaa tgcagccctc cggctctccg 50
cgaagaagtt ccctgccccg atgagccccc gccgtgcgtc cccgactatc 100
cccaggcgaa cgtggggcac cgggcccagc gccgacgatc gctgccgtt 150
tgcccttggg agtaggatgt ggtgaaagga tggggcttct cccttacggg 200
gctcacaatg gccagagaag attccgtgaa gtgtctgcgc tgcctgctct 250
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35 40 45

Thr Ala Glu Thr Arg Val Glu Glu Ala Val Ile Leu Thr Tyr Phe
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Pro Val Val His Pro Val Met Ile Ala Val Cys Cys Phe Leu Ile
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Ile Val Gly Met Leu Gly Tyr Cys Gly Thr Val Lys Arg Asn Leu
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Leu Leu Leu Ala Trp Tyr Phe Gly Ser Leu Leu Val Ile Phe Cys
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Val Glu Leu Ala Cys Gly Val Trp Thr Tyr Glu Gln Glu Leu Met
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Val Pro Val Gln Trp Ser Asp Met Val Thr Leu Lys Ala Arg Met
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Thr Asn Tyr Gly Leu Pro Arg Tyr Arg Trp Leu Thr His Ala Trp
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Asn Phe Phe Gln Arg Glu Phe Lys Cys Cys Gly Val Val Tyr Phe
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Cys Cys Val Arg Glu Phe Pro Gly Cys Ser Lys Gln Ala His Gln
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Glu Asp Leu Ser Asp Leu Tyr Gln Glu Gly Cys Gly Lys Lys Met
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Tyr Ser Phe Leu Arg Gly Thr Lys Gln Leu Gln Val Leu Arg Phe
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Thr Ile Thr Leu Leu Trp Ala Leu Tyr Tyr Asp Arg Arg Glu Pro
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Gly Thr Asp Gln Met Met Ser Leu Lys Asn Asp Asn Ser Gln His
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